

152241

Delaval, Jan

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**From:** Liu, Samuel  
**Sent:** Monday, May 02, 2005 3:56 PM  
**To:** Delaval, Jan  
**Subject:** 10749387

Hi, Jan,

Please conduct search for the amino acid sequence of SEQ ID NO:1 against commercial protein and interference databases for application 10749387 east 50 search results, as timely concerned:

Very best,

Samuel Liu  
AU 1653, REM 3C84  
571-272-0949

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:06 ; Search time 74 Seconds  
(without alignments)  
658.538 Million cell updates/sec

Title: US-10-749-387-1

Perfect score: 695  
Sequence: 1 DLBCPSGWSSTDRYCYKPKF.....WPKVDCGQHSHCKFTRRP 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 65 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	98.4	126	2 AAR71979	Aar71979 Snake ven
2	684	98.4	126	3 AAY85627	Aay85627 Snake ven
3	684	98.4	126	5 AAO20973	Aao20973 126-mer w
4	684	98.4	149	2 AAR71981	Aar71981 Snake ven
5	684	98.4	149	3 AAY85628	Aay85628 Snake ven
6	684	98.4	149	5 AAO20974	Aao20974 149-mer w
7	678	97.6	126	5 AAO20983	Aao20983 M10-G4 K6
8	678	97.6	126	5 AAO20990	Aao20990 M17-G4 R1
9	678	97.6	126	5 AAO20986	Aao20986 M13-G4 R6
10	678	97.6	126	5 AAO20991	Aao20991 M18-G4 R1
11	678	97.6	126	5 AAO20988	Aao20988 M15-G4 R1
12	678	97.6	126	5 AAO20980	Aao20980 M7-G4 K20
13	678	97.6	126	5 AAO20984	Aao20984 M11-G4 E6
14	678	97.6	126	5 AAO20992	Aao20992 M19-G4 E1
15	678	97.3	126	5 AAO20989	Aao20989 M16-G4 D1
16	678	97.3	126	5 AAO20993	Aao20993 M20-G4 F1
17	678	97.3	126	5 AAO20981	Aao20981 M8-G4 D54
18	675	97.1	126	5 AAO20985	Aao20985 M12-G4 Y6
19	675	97.1	126	5 AAO20987	Aao20987 M14-G4 Y6
20	675	97.1	126	5 AAO20982	Aao20982 M9-G4 Y58
21	673	96.8	126	5 AAO20998	Aao20998 M25-G4 D1
22	673	96.5	126	5 AAO20996	Aao20996 M23-G4 D5
23	670	96.4	126	5 AAO20999	Aao20999 M26-G4 D5
24	668	96.1	126	5 AAO20997	Aao20997 M24-G4 D5
25	668	96.1	126	5 AAO20994	Aao20994 M21-G4 D5

26	662	95.3	126	5 AAO20995	Aao20995 M22-G4 D5
27	661	95.1	127	2 AAR24426	Aar24426 Sequence
28	551	79.3	110	5 AAO20975	Aao20975 110-mer c
29	361.5	52.0	158	5 AAE20181	Aae20181 Pigmy rat
30	340.5	49.0	130	2 AAR38228	Aar38228 Sequence
31	322.5	46.4	132	2 AAR38226	Aar38226 Sequence
32	318.5	45.8	131	2 AAR38222	Aar38222 Sequence
33	316.5	45.5	144	5 AAE20180	Aae20180 Pigmy rat
34	314.5	45.3	152	5 AAE20179	Aae20179 Pigmy rat
35	311	44.7	133	2 AAR45156	Aar45156 Botrocetl
36	307.5	44.2	134	2 AAR38223	Aar38223 Sequence
37	304.5	43.8	154	5 AAO14520	Aao14520 Korean ad
38	292.5	42.1	152	4 AAM51543	Aam51543 Snake ven
39	274	39.4	132	5 AAB79130	Aab79130 Anylytant
40	271.5	39.1	129	6 ABU08798	Abu08798 Deinagkis
41	271.5	39.1	129	7 ABU62534	Abu62534 Snake ant
42	262.5	37.8	132	2 AAR72235	Aar72235 Vipera pa
43	256.5	36.9	133	2 AAR38230	Aar38230 Sequence
44	243.5	35.0	123	2 AAR38225	Aar38225 Sequence
45	226.5	32.6	127	2 AAR72236	Aar72236 Vipera pa
46	210.5	30.3	146	4 AAM51544	Aam51544 Snake ven
47	210.5	30.3	146	6 ABU08799	Abu08799 Deinagkis
48	210.5	30.3	146	7 ABU62539	Abu62539 Snake ant
49	209	30.1	116	2 AAR24427	Aar24427 Sequence
50	208	29.9	38	2 AAR71978	Aar71978 Snake ven
51	201.5	29.0	123	5 AAB79131	Abb79131 Anylytant
52	200	28.8	107	2 AAR38227	Aar38227 Sequence
53	198	28.5	145	5 AAO14521	Aao14521 Korean ad
54	197	28.3	36	2 AAR3885	Aar3885 N-termina
55	191.5	27.6	125	2 AAR45157	Aar45157 Botrocetl
56	188.5	27.1	125	2 AAR38224	Aar38224 Sequence
57	184.5	26.5	151	5 AAE20178	Aae20178 Pigmy rat
58	176	25.3	120	5 ABB83143	Abb83143 Anylytant
59	174	25.0	166	1 AAB81514	Aab81514 Sequence
60	172.5	24.8	34	5 AAO20977	Aao20977 Peptide f
61	172	24.7	44	3 AAY85632	Aay85632 Snake ven
62	172	24.7	165	1 AAP94614	Aap94614 Human reg
63	168	24.2	133	2 AAR66593	Aar66593 Human reg
64	168	24.2	144	2 AAR66592	Aar66592 Human reg
65	168	24.2	146	2 AAR66591	Aar66591 Human reg

## ALIGNMENTS

RESULT 1	AAR71979	standard; peptide; 126 AA.
ID	AAR71979	
XX	AAR71979;	
AC	25-MAR-2003 (revised)	
XX	28-NOV-1995 (first entry)	
DT	Snake venom derived antithrombotic peptide.	
XX	Antithrombotic peptide; snake venom; platelet binding inhibition;	
KW	von Willebrand factors; Crocatus horridus horridus.	
XX	Crocatus horridus horridus.	
OS	Key	Location/Qualifiers
XX	Disulfide-bond 4..15	
FT	Disulfide-bond 32..120	
FT	Disulfide-bond 95..112	
PN	MO9508573-AI.	
XX	30-MAR-1995.	
PD	21-SEP-1994;	94MO-JP001555.
XX	22-SEP-1993;	93JP-00236975.

XX (AJIN ) AJINOMOTO KK.  
PA  
XX  
PI Fukuchi N, Yamamoto H, Nagano M, Kito M, Tanaka A, Ishii K;  
PI Kobayashi T, Yoshimoto R;  
XX  
DR WPI; 1995-139559/18.  
XX  
PT Single-chain antithrombotic peptide - obtained by cleaving an  
PT oligopeptide from snake venom to break inter-chain di-sulphide bonds but  
PT preserve intra-chain di-sulphide bonds.  
XX  
PS Claim 3; Page 44-45; 84pp; Japanese.  
XX  
CC AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,  
CC prepared by cleaving the interpeptide but retaining the intrapeptide  
CC disulphide bonds of the original snake venom oligopeptide. These peptides  
CC have the advantage of avoiding significant thrombocytopenia when  
CC administered at the minimum dose, for in vivo inhibition of platelet von  
CC Willebrand factor binding. (Updated on 25-MAR-2003 to correct PN field.)  
CC  
XX  
SQ Sequence 126 AA;

Query Match 98.4%; Score 684; DB 2; Length 126;  
Best Local Similarity 98.4%; Pred. No. 1.5e-71;  
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIECPGSGMSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDNLTLYAN 60  
DB 1 DIECPGSGMSYDRYCYKPFKQEMTWADAEKFCSEQAKGHLISVETALASFPDNLVLYAN 60  
QY 61 KEYLTRYIWIIGLRVONKGPCCSSISYENLVDPFECFMSRDTLRLEWFKVDCQOHSFIC 120  
DB 61 KEYLTRYIWIIGLRVONKGPCCSSISYENLVDPFECFMSRDTLRLEWFKVDCQOHSFIC 120

QY 121 KFTRRP 126  
DB 121 KFTRRP 126

RESULT 2  
AAV85627  
ID AAV85627 standard; protein; 126 AA.

XX  
AC AAV85627;

DT 07-FEB-2001 (first entry)

DE Snake venom derived protein.

XX  
KM Subunit peptide production; snake venom; rattlesnake; thrombolytic;  
KM von Willebrand's factor; blood platelet-inhibitory activity.

OS Crotalus horridus horridus.

PN W0200059926-A1.

PD 12-OCT-2000.

PF 31-MAR-2000; 2000WO-JP002127.

PR 02-APR-1999; 99JP-00096073.

PA (AJIN ) AJINOMOTO CO INC.

PI Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;

DR WPI; 2000-664985/64.

XX  
PT Producing physiologically-active subunit peptides originating in polymer  
PT proteins by denaturation and specific separation, with lower antigenicity  
PT but improved solubility and stability, e.g. blood platelet-binding  
PT inhibitors.

XX  
PS Claim 15; Page 44; 51pp; Japanese.

CC This invention relates to a method for the production of a subunit  
CC peptide originating from a polymer protein with disulphide bonds within  
CC and between subunits. The method comprises denaturing the protein or its  
CC subunit using a protein denaturing agent in a solution, removing the  
CC agent in the presence of a polyoxalkyl polyether which reacts with a  
CC thiol group and unwinds the subunit, and separating the polyoxalkyl  
CC polyether-bound subunit peptide. The method can be used for producing  
CC physiologically-active subunit peptides for polymer proteins e.g. snake  
CC venom-originated dimer peptide with blood platelet-inhibitory activity on  
CC von Willebrand's factor. The peptides produced have platelet-binding  
CC inhibitory, and thrombolytic activity. The present sequence represents a  
CC invention

XX  
SQ Sequence 126 AA;

Query Match 98.4%; Score 684; DB 3; Length 126;  
Best Local Similarity 98.4%; Pred. No. 1.5e-71;  
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIECPGSGMSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDNLTLYAN 60  
DB 1 DIECPGSGMSYDRYCYKPFKQEMTWADAEKFCSEQAKGHLISVETALASFPDNLVLYAN 60

QY 61 KEYLTRYIWIIGLRVONKGPCCSSISYENLVDPFECFMSRDTLRLEWFKVDCQOHSFIC 120  
DB 61 KEYLTRYIWIIGLRVONKGPCCSSISYENLVDPFECFMSRDTLRLEWFKVDCQOHSFIC 120

QY 121 KFTRRP 126  
DB 121 KFTRRP 126

RESULT 3  
AAO20973  
ID AAO20973 standard; protein; 126 AA.

XX  
AC AAO20973;

DT 19-JUL-2002 (first entry)

DE 126-mer wild-type rattlesnake protein.

XX  
KM Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
KM drug efficacy.

OS Crotalus horridus horridus.

PN EP1195384-A1.

PD 10-APR-2002.

PF 04-OCT-2001; 2001EP-00123277.

PR 04-OCT-2000; 2000JP-00305279.

PA (AJIN ) AJINOMOTO CO INC.

PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;

DR Gendoh K, Shinda N, Yamada N;

DR WPI; 2002-364482/40.

XX  
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,  
PT comprises specific mutations in protein originating from snake venom.  
XX Claim 1; Page 25; 49pp; English.

XX  
CC The invention relates to a glycoprotein Ib-binding protein, originating



CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC antithrombotic AS1051 126-mer wild-type rattlesnake protein of the  
 CC invention

XX Sequence 126 AA;

Query Match 98.4%; Score 684; DB 5; Length 126;  
 Best Local Similarity 98.4%; Pred. No. 1.5e-71;  
 Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPKFQKEMTWASARFCSEQAKGHLISVETALASFPDNYLYAN 60  
 DB 1 DLECPGMSSTDRYCYKPKFQKEMTWADARFCSEQAKGHLISVETALASFPDNYLYAN 60  
 QY 61 KEYLTRYIWIIGLRVQKQPCSSISYENLVDPFECFVMSRDTLRREMFKVDCEQHSFIC 120  
 DB 61 KEYLTRYIWIIGLRVQKQPCSSISYENLVDPFECFVMSRDTLRREMFKVDCEQHSFIC 120  
 QY 121 KFTRRPR 126  
 DB 121 KFTRRPR 126

#### RESULT 4

AA71981  
 ID AAR71981 standard; protein; 149 AA.

AC AAR71981;  
 DT 25-MAR-2003 (revised)  
 DT 28-NOV-1995 (first entry)  
 DE Snake venom antithrombotic oligopeptide.  
 DE Antithrombotic peptide; snake venom; platelet binding inhibition;  
 KW von Willebrand factor; Crotalus horridus horridus.  
 OS Crotalus horridus horridus.

Key Location/Qualifiers  
 FT Disulfide-bond 27..38  
 FT Disulfide-bond 55..143  
 FT Disulfide-bond 118..135

PN W09508573-A1.  
 PD 30-MAR-1995.

PF 21-SEP-1994; 94WO-JP001555.

PR 22-SEP-1993; 93JP-00236975.

PA (AJIN) AJINOMOTO KK.

PI Fukuchi N, Yamamoto H, Nagano M, Kito M, Tanaka A, Ishii K,  
 PI Kobayashi T, Yoshimoto R,

DR WPI; 1995-139559/18.  
 DR N-PSDB; AAO89309.

XX Single-chain antithrombotic peptide - obtained by cleaving an  
 PT oligopeptide from snake venom to break inter-chain di-sulphide bonds but  
 PT preserve intra-chain di-sulphide bonds.

PS Example 2; Page 47-48; 84pp; Japanese.

XX AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,  
 CC specifically from the snake venom oligopeptide AAR71981, encoded by  
 CC AAO89309. These peptides have the advantage of avoiding significant

CC thrombocytopenia when administered at the minimum dose, for in vivo  
 CC inhibition of platelet von Willebrand factor binding. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 149 AA;

Query Match 98.4%; Score 684; DB 2; Length 149;  
 Best Local Similarity 98.4%; Pred. No. 1.8e-71;  
 Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPKFQKEMTWASARFCSEQAKGHLISVETALASFPDNYLYAN 60  
 DB 24 DLECPGMSSTDRYCYKPKFQKEMTWADARFCSEQAKGHLISVETALASFPDNYLYAN 83  
 QY 61 KEYLTRYIWIIGLRVQKQPCSSISYENLVDPFECFVMSRDTLRREMFKVDCEQHSFIC 120  
 DB 84 KEYLTRYIWIIGLRVQKQPCSSISYENLVDPFECFVMSRDTLRREMFKVDCEQHSFIC 143  
 QY 121 KFTRRPR 126  
 DB 144 KFTRRPR 149

#### RESULT 5

AA85628  
 ID AAY85628 standard; protein; 149 AA.

AC AAY85628;  
 DT 07-FEB-2001 (first entry)  
 DE Snake venom derived protein.

KW Subunit peptide production; snake venom; rattlesnake; thrombolytic;  
 KW von Willebrand's factor; blood platelet-inhibitory activity.  
 OS Crotalus horridus horridus.

PN W0200059926-A1.

PD 12-OCT-2000.

PF 31-MAR-2000; 2000WO-JP002127.

PR 02-APR-1999; 99JP-00096073.

PA (AJIN) AJINOMOTO CO INC.

PI Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;

DR WPI; 2000-664985/64.

DR N-PSDB; AAC61144.

PT Producing physiologically-active subunit peptides originating in polymer  
 PT proteins by denaturation and specific separation, with lower antigenicity  
 PT but improved solubility and stability, e.g. blood platelet-binding  
 PT inhibitors.

PS Example 2; Page 47; 51pp; Japanese.

XX This invention relates to a method for the production of a subunit  
 CC peptide originating from a polymer protein with disulphide bonds within  
 CC and between subunits. The method comprises denaturing the protein or its  
 CC subunit using a protein denaturing agent in a solution, removing the  
 CC agent in the presence of a polyoxalkyl polyether which reacts with a  
 CC thiol group and unwinds the subunit, and separating the polyoxalkyl  
 CC polyether-bound subunit peptide. The method can be used for producing  
 CC physiologically-active subunit peptides for polymer proteins e.g. snake  
 CC venom-originated dimer peptide with blood platelet-inhibitory activity on  
 CC von Willebrand's factor. The peptides produced have platelet-binding  
 CC inhibitory, and thrombolytic activity. The present sequence represents a  
 CC rattlesnake protein used in an example illustrating the method of the  
 CC invention

XX Sequence 149 AA;  
 SQ Query Match 98.4%; Score 684; DB 3; Length 149;  
 Best Local Similarity 98.4%; Pred. No. 1.8e-71;  
 Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 60  
 DB 24 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 83

QY 61 KEYLTRYIWIGLRVONKQPCSSISYENLVDFEFCFMSRDLRLRMFVKVDCQOHSFIC 120  
 DB 84 KEYLTRYIWIGLRVONKQPCSSISYENLVDFEFCFMSRDLRLRMFVKVDCQOHSFIC 143

QY 121 KFTRRP 126  
 DB 144 KFTRRP 149

## RESULT 6

AAO20974  
 ID AAO20974 standard; protein; 149 AA.

AC AAO20974;

DT 19-JUL-2002 (first entry)

DE 149-mer wild-type rattlesnake protein.

XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy.

OS Crotales horridus horridus.

XX EP1195384-A1.

XX 10-APR-2002.

XX 04-OCT-2001; 2001EP-00123277.

XX 04-OCT-2000; 2000JP-00305279.

XX (AJIN) AJINOMOTO CO INC.

PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
 PI Gondoh K, Shinda N, Yamada N;

DR WPI; 2002-364482/40.

DR N-PSDB; AAK99834.

XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.

XX Example 1; Page 26-27; 49pp; English.

XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC antithrombotic 149-mer wild-type rattlesnake protein of the invention

XX Sequence 149 AA;

Query Match 98.4%; Score 684; DB 5; Length 149;

Best Local Similarity 98.4%; Pred. No. 1.8e-71;  
 Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 60

DB 24 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 83  
 QY 61 KEYLTRYIWIGLRVONKQPCSSISYENLVDFEFCFMSRDLRLRMFVKVDCQOHSFIC 120  
 DB 84 KEYLTRYIWIGLRVONKQPCSSISYENLVDFEFCFMSRDLRLRMFVKVDCQOHSFIC 143

QY 121 KFTRRP 126  
 DB 144 KFTRRP 149

## RESULT 7

AAO20983  
 ID AAO20983 standard; protein; 126 AA.

AC AAO20983;

DT 19-JUL-2002 (first entry)

DE M10-G4 K61A mutant of the antithrombotic rattlesnake protein.

XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy; mutant; mutein.

OS Crotales horridus horridus.  
 OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 61 /note= "wild-type Lys substituted by Ala"

XX EP1195384-A1.

XX 10-APR-2002.

XX 04-OCT-2001; 2001EP-00123277.

XX 04-OCT-2000; 2000JP-00305279.

XX (AJIN) AJINOMOTO CO INC.

PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
 PI Gondoh K, Shinda N, Yamada N;

DR WPI; 2002-364482/40.

XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.

XX Example 4; Page; 49pp; English.

XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC K61A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 CC protein of the invention. NOTE: This mutant protein sequence is not shown  
 CC in the specification. It has been created from information provided in  
 CC Example 4

XX Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;

Best Local Similarity 97.6%; Pred. No. 7.4e-71;  
 Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 60

DB 1 DIECPGWSYDRYCYKPFQKQEMTWASAEKFCSEQAKGHLISVETALEASFVDNVLVYAN 60

Qy 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120  
 Db 61 AEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120  
 Qy 121 KFTTRPR 126  
 Db 121 KFTTRPR 126

## RESULT 8

AAO20990 standard; protein; 126 AA.

AAO20990; 19-JUL-2002 (first entry)

M17-G4 R103A mutant of the antithrombotic rattlesnake protein.

Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 drug efficacy; mutant; mutein.  
 Crotalus horridus horridus.  
 Synthetic.

Key Location/Qualifiers

Misc-difference 103 /note= "Wild-type Arg substituted by Ala"

EP1195384-A1.

10-APR-2002.

04-OCT-2001; 2001EP-00123277.

04-OCT-2000; 2000JP-00305279.

(AJIN ) AJINOMOTO CO INC.

Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,  
 Gondoh K, Shimba N, Yamada N;

WPI; 2002-364482/40.

Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 comprises specific mutations in protein originating from snake venom.

Example 4; Page; 49pp; English.

The invention relates to a glycoprotein Ib-binding protein, originating  
 from snake venom, comprising specific mutations and antithrombotic  
 activity. Glycoprotein Ib-binding protein is used in a drug having  
 antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 binding activity to glycoprotein Ib, a long half life/drug efficacy  
 retention in blood, and low antigenicity. This sequence represents the  
 R103A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 protein of the invention. NOTE: This mutant protein sequence is not shown  
 in the specification. It has been created from information provided in  
 Example 4

Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;

Best Local Similarity 97.6%; Pred. No. 7,4e-71; Indels 0; Gaps 0;

Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFDVNTLYAN 60  
 Db 1 DLECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFDVNTLYAN 60  
 Qy 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120  
 Db 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120

Db 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120  
 Qy 121 KFTTRPR 126  
 Db 121 KFTTRPR 126

## RESULT 9

AAO20986 standard; protein; 126 AA.

AAO20986; 19-JUL-2002 (first entry)

M13-G4 R66A mutant of the antithrombotic rattlesnake protein.

Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 drug efficacy; mutant; mutein.  
 Crotalus horridus horridus.  
 Synthetic.

Key Location/Qualifiers

Misc-difference 66 /note= "Wild-type Arg substituted by Ala"

EP1195384-A1.

10-APR-2002.

04-OCT-2001; 2001EP-00123277.

04-OCT-2000; 2000JP-00305279.

(AJIN ) AJINOMOTO CO INC.

Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,  
 Gondoh K, Shimba N, Yamada N;

WPI; 2002-364482/40.

Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 comprises specific mutations in protein originating from snake venom.

Example 4; Page; 49pp; English.

The invention relates to a glycoprotein Ib-binding protein, originating  
 from snake venom, comprising specific mutations and antithrombotic  
 activity. Glycoprotein Ib-binding protein is used in a drug having  
 antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 binding activity to glycoprotein Ib, a long half life/drug efficacy  
 retention in blood, and low antigenicity. This sequence represents the  
 R66A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 protein of the invention. NOTE: This mutant protein sequence is not shown  
 in the specification. It has been created from information provided in  
 Example 4

Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;

Best Local Similarity 97.6%; Pred. No. 7,4e-71; Indels 0; Gaps 0;

Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFDVNTLYAN 60  
 Db 1 DLECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFDVNTLYAN 60  
 Qy 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120  
 Db 61 KEYLTRYIMIGLRVQNGKQPCSSISYENLVDPPECVMSRDTLRLEWFKVDCEQHSFIC 120

QY 121 KFTRR 126  
 |||||  
 DB 121 KFTRR 126

## RESULT 10

AAO20991  
 ID AAO20991 standard; protein; 126 AA.

AC AAO20991;  
 XX  
 DT 19-JUL-2002 (first entry)

XX M18-G4 R105A mutant of the antithrombotic rattlesnake protein.

XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy; mutant; mutein.

XX Crotalus horridus horridus.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Misc-difference 105 /note="Wild-type Arg substituted by Ala"

PN EPI195384-A1.

PD 10-APR-2002.

PF 04-OCT-2001; 2001EP-00123277.

PR 04-OCT-2000; 2000JP-00305279.

XX (AJIN ) AJINOMOTO CO INC.

PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
 PI Gondo K, Shimba N, Yamada N;

DR WPI; 2002-364482/40.

XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.

XX Example 4; Page; 49pp; English.

XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC R105A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 CC protein of the invention. NOTE: This mutant protein sequence is not shown  
 CC in the specification. It has been created from information provided in  
 CC Example 4

XX Sequence 126 AA;

QY Query Match 97.6%; Score 678; DB 5; Length 126;  
 Best Local Similarity 97.6%; Pred. No. 7.4e-71;  
 Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPFKQEMTWASAEKFCSEQAKGGHLLSVETALBASFDVNLVYAN 60  
 |||||

DB 1 DLECPGMSSTDRYCYKPFKQEMTWADAEKFCSEQAKGGHLLSVETALBASFDVNLVYAN 60  
 |||||

QY 61 KEYLTRYIWIIGLRVONKGGPCSSISYENLVDPFECFVMSADTRLRMEFKVDCQGHSHFIC 120  
 |||||

DB 61 KEYLTRYIWIIGLRVONKGGPCSSISYENLVDPFECFVMSADTRLRMEFKVDCQGHSHFIC 120  
 |||||

QY 121 KFTRR 126  
 |||||

DB 121 KFTRR 126

## RESULT 11

AAO20988  
 ID AAO20988 standard; protein; 126 AA.

AC AAO20988;  
 XX  
 DT 19-JUL-2002 (first entry)

XX M15-G4 R100A mutant of the antithrombotic rattlesnake protein.

XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy; mutant; mutein.

XX Crotalus horridus horridus.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Misc-difference 100 /note="Wild-type Arg substituted by Ala"

PN EPI195384-A1.

PD 10-APR-2002.

PF 04-OCT-2001; 2001EP-00123277.

PR 04-OCT-2000; 2000JP-00305279.

XX (AJIN ) AJINOMOTO CO INC.

PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
 PI Gondo K, Shimba N, Yamada N;

DR WPI; 2002-364482/40.

XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.

XX Example 4; Page; 49pp; English.

XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC R100A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 CC protein of the invention. NOTE: This mutant protein sequence is not shown  
 CC in the specification. It has been created from information provided in  
 CC Example 4

XX Sequence 126 AA;

QY Query Match 97.6%; Score 678; DB 5; Length 126;  
 Best Local Similarity 97.6%; Pred. No. 7.4e-71;  
 Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPFKQEMTWASAEKFCSEQAKGGHLLSVETALBASFDVNLVYAN 60  
 |||||

DB 1 DLECPGMSSTDRYCYKPFKQEMTWADAEKFCSEQAKGGHLLSVETALBASFDVNLVYAN 60  
 |||||

QY 61 KEYLTRYIWIIGLRVONKGGPCSSISYENLVDPFECFVMSADTRLRMEFKVDCQGHSHFIC 120  
 |||||

DB 61 KEYLTRYIWIIGLRVONKGGPCSSISYENLVDPFECFVMSADTRLRMEFKVDCQGHSHFIC 120  
 |||||

QY 121 KFTRR 126  
 |||||

DB 121 KFTRR 126

## RESULT 12

AAO20980 standard; protein; 126 AA.

AAO20980;

19-JUL-2002 (first entry)

M7-G4 K20A mutant of the antithrombotic rattlesnake protein.

Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
drug efficacy; mutant; mutein.

Crotalus horridus horridus.  
Synthetic.

Key Location/Qualifiers

FT Misc-difference 20 /note= "Wild-type Lys substituted by Ala"

EP1195384-A1.

10-APR-2002.

04-OCT-2001; 2001EP-00123277.

04-OCT-2000; 2000JP-00305279.

(AJIN) AJINOMOTO CO INC.

Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;

Gondoh K, Shiba N, Yamada N;

WPI; 2002-364482/40.

Glycoprotein Ib-binding protein, useful for treating thrombosis,

comprises specific mutations in protein originating from snake venom.

Example 4; Page: 49pp; English.

The invention relates to a glycoprotein Ib-binding protein, originating

from snake venom, comprising specific mutations and antithrombotic

activity. Glycoprotein Ib-binding protein is used in a drug having

antithrombotic activity. Glycoprotein Ib-binding protein has a high

binding activity to glycoprotein Ib, a long half life/drug efficacy

retention in blood, and low antigenicity. This sequence represents the

K20A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake

protein of the invention. NOTE: This mutant protein sequence is not shown

in the specification. It has been created from information provided in

Example 4

Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;

Best Local Similarity 97.6%; Pred. No. 7.4e-71;

Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## RESULT 13

AAO20984 standard; protein; 126 AA.

AAO20984;

19-JUL-2002 (first entry)

M11-G4 B62A mutant of the antithrombotic rattlesnake protein.

Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
drug efficacy; mutant; mutein.

Crotalus horridus horridus.  
Synthetic.

Key Location/Qualifiers

FT Misc-difference 62 /note= "Wild-type Glu substituted by Ala"

EP1195384-A1.

10-APR-2002.

04-OCT-2001; 2001EP-00123277.

04-OCT-2000; 2000JP-00305279.

(AJIN) AJINOMOTO CO INC.

Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;

Gondoh K, Shiba N, Yamada N;

WPI; 2002-364482/40.

Glycoprotein Ib-binding protein, useful for treating thrombosis,

comprises specific mutations in protein originating from snake venom.

Example 4; Page: 49pp; English.

The invention relates to a glycoprotein Ib-binding protein, originating

from snake venom, comprising specific mutations and antithrombotic

activity. Glycoprotein Ib-binding protein is used in a drug having

antithrombotic activity. Glycoprotein Ib-binding protein has a high

binding activity to glycoprotein Ib, a long half life/drug efficacy

retention in blood, and low antigenicity. This sequence represents the

B62A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake

protein of the invention. NOTE: This mutant protein sequence is not shown

in the specification. It has been created from information provided in

Example 4

Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;

Best Local Similarity 97.6%; Pred. No. 7.4e-71;

Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## RESULT 14

AAO20992 standard; protein; 126 AA.

```

XX AC AAO20992;
XX DT 19-JUL-2002 (first entry)
XX DE M19-G4 E106A mutant of the antithrombotic rattlesnake protein.
XX KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
XX KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
XX KW drug efficacy; mutant; mutein.
XX OS Crocalus horridus horridus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT M19-G4 difference 106 /note="Wild-type Glu substituted by Ala"
XX FT EPI195384-A1.
XX PN 10-APR-2002.
XX PD 04-OCT-2001; 2001EP-00123277.
XX PF 04-OCT-2000; 2000JP-00305279.
XX PR (AJIN ) AJINOMOTO CO INC.
XX PA Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
XX PI Gondoh K, Shinda N, Yamada N;
XX DR WPI; 2002-364482/40.
XX DT Glycoprotein Ib-binding protein, useful for treating thrombosis,
XX PT comprises specific mutations in protein originating from snake venom.
XX PS Example 4; Page: 49pp; English.
XX CC The invention relates to a glycoprotein Ib-binding protein, originating
XX CC from snake venom, comprising specific mutations and antithrombotic
XX CC activity. Glycoprotein Ib-binding protein is used in a drug having
XX CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
XX CC binding activity to glycoprotein Ib, a long half life/drug efficacy
XX CC retention in blood, and low antigenicity. This sequence represents the
XX CC E106A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
XX CC protein of the invention. NOTE: This mutant protein sequence is not shown
XX CC in the specification. It has been created from information provided in
XX CC Example 4
XX SQ Sequence 126 AA;
XX
Query Match 97.6%; Score 678; DB 5; Length 126;
Best Local Similarity 97.6%; Pred. No. 7.4e-71;
Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIECPGMSSTDRYCYKPKFQKQMTWASAEFCSEQAKGHLISVETALASFDVNTLYAN 60
DB 1 DIECPGMSSTDRYCYKPKFQKQMTWADAEFCSEQAKGHLISVETALASFDVNTLYAN 60
QY 61 KEVLTIRYIWIGLRVQKQGPCSSISYENLVDPFECFVMSRDTLRERMFVKVDCQCHSFTIC 120
DB 61 KEVLTIRYIWIGLRVQKQGPCSSISYENLVDPFECFVMSRDTLRERMFVKVDCQCHSFTIC 120
QY 121 KFTTRPR 126
DB 121 KFTTRPR 126

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XX AC AAO20993;
XX DT 19-JUL-2002 (first entry)
XX DE M16-G4 D101A mutant of the antithrombotic rattlesnake protein.
XX KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
XX KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
XX KW drug efficacy; mutant; mutein.
XX OS Crocalus horridus horridus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT M16-G4 difference 101 /note="Wild-type Asp substituted by Ala"
XX FT EPI195384-A1.
XX PN 10-APR-2002.
XX PD 04-OCT-2001; 2001EP-00123277.
XX PF 04-OCT-2000; 2000JP-00305279.
XX PR (AJIN ) AJINOMOTO CO INC.
XX PA Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
XX PI Gondoh K, Shinda N, Yamada N;
XX DR WPI; 2002-364482/40.
XX DT Glycoprotein Ib-binding protein, useful for treating thrombosis,
XX PT comprises specific mutations in protein originating from snake venom.
XX PS Example 4; Page: 49pp; English.
XX CC The invention relates to a glycoprotein Ib-binding protein, originating
XX CC from snake venom, comprising specific mutations and antithrombotic
XX CC activity. Glycoprotein Ib-binding protein is used in a drug having
XX CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
XX CC binding activity to glycoprotein Ib, a long half life/drug efficacy
XX CC retention in blood, and low antigenicity. This sequence represents the
XX CC D101A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
XX CC protein of the invention. NOTE: This mutant protein sequence is not shown
XX CC in the specification. It has been created from information provided in
XX CC Example 4
XX SQ Sequence 126 AA;
XX
Query Match 97.3%; Score 676; DB 5; Length 126;
Best Local Similarity 97.6%; Pred. No. 1.3e-70;
Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIECPGMSSTDRYCYKPKFQKQMTWASAEFCSEQAKGHLISVETALASFDVNTLYAN 60
DB 1 DIECPGMSSTDRYCYKPKFQKQMTWADAEFCSEQAKGHLISVETALASFDVNTLYAN 60
QY 61 KEVLTIRYIWIGLRVQKQGPCSSISYENLVDPFECFVMSRDTLRERMFVKVDCQCHSFTIC 120
DB 61 KEVLTIRYIWIGLRVQKQGPCSSISYENLVDPFECFVMSRDTLRERMFVKVDCQCHSFTIC 120
QY 121 KFTTRPR 126
DB 121 KFTTRPR 126

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RESULT 15  
 AAO20989  
 ID AAO20989 standard; protein; 126 AA.  
 AC AAO20989;

RESULT 16  
 AAO20993  
 ID AAO20993 standard; protein; 126 AA.  
 AC AAO20993;  
 DT 19-JUL-2002 (first entry)

Query	Match	Similarity	Score	DB	Length	Match	Local	Conservative	Mismatches	Indels	Gaps
QY	1	DLECPGSGSTDRYCYKPKFQEMTWASARFCSEQAKGHLSTVETALEASFDVNVLYAN	97.3%	676	5	126	Beet	123	0	3	0
DB	1	DLECPGSGSTDRYCYKPKFQEMTWADARFCSEQAKGHLSTVETALEASFDVNVLYAN	97.6%	676	5	126	Matches	123	0	3	0
QY	61	KEYLTRYIWMIGLRVONKQPCSSISYENVLPDFECFMYSRDTRLRLMEKRVDCQGHSPIC	120								
DB	61	KEYLTRYIWMIGLRVONKQPCSSISYENVLPDFECFMYSRDTRLRLMEKRVDCQGHSPIC	120								
QY	121	KETPRR	126								
DB	121	KETPRR	126								

RESULT 17

AAO20981

AAO20981 standard; protein, 126 AA.

AAO20981;

19-JUL-2002 (first entry)

M8-G4 D54A mutant of the antithrombotic rattlesnake protein.

KX	Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW	antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KM	drug efficacy; mutant; mutein.
XX	
OS	Crotalus horridus horridus.
XX	Synthetic.
FT	Key Location/Qualifiers
FT	Misc-difference 54 /note= "wild-type Asp substituted by Ala"
PN	BPII95384-A1.
PD	10-APR-2002.
XX	
PP	04-OCT-2001; 2001EP-00123277.
PR	04-OCT-2000; 2000JP-00305279.
PA	(AJIN ) AJINOMOTO CO INC.
P1	Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
P1	Gondoh K, Shimba N, Yamada N;
DR	WPI; 2002-364482/40.
XX	
PT	Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT	comprises specific mutations in protein originating from snake venom.
XX	
PS	Example 4; Page; 4pp; English.
XX	
CC	The invention relates to a glycoprotein Ib-binding protein, originating
CC	from snake venom, comprising specific mutations and antithrombotic
CC	activity. Glycoprotein Ib-binding protein is used in a drug having
CC	antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC	binding activity to glycoprotein Ib, a long half life/drug efficacy
CC	retention in blood, and low antigenicity. This sequence represents the
CC	D5A4 mutant of the antithrombotic As1051 126-mer wild-type rattlesnake
CC	protein of the invention. NOTE: This mutant protein sequence is not shown
CC	in the specification. It has been created from information provided in
CC	Example 4
XX	
SO	Sequence 126 AA;
QY	Query Match 97.3%; Score 676; DB 5; Length 126; Best Local Similarity 97.6%; Pred. No. 1.3e-70; Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB	1 DLBCPSGMSSTDRCYKPFKQEMTWASAEFCSOAKGHLLSVETALIASFDNVLTYAN 60 1 DLBCPSGMSSTDRCYKPFKQEMTWADAEPCSSOAKGHLLSVETALIASFDNVLTYAN 60
OY	61 KEVTRTRYIMGLARONQGQPCSSISYENVLDPEFCFVWSRPTRLREMPKYDCEQHSPIC 120 61 KEVTRTRYIMGLARONKGQPCSSISYENVLDPEFCFVWSRPTRLREMPKYDCEQHSPIC 120
DB	61 KEVTRTRYIMGLARONKGQPCSSISYENVLDPEFCFVWSRPTRLREMPKYDCEQHSPIC 120 61 KEVTRTRYIMGLARONKGQPCSSISYENVLDPEFCFVWSRPTRLREMPKYDCEQHSPIC 120
OY	121 KETRPR 126     121 KETRPR 126
DE	RESULT 18 ID AAO20985 standard; protein; 126 AA. AC AAO20985, DT 19-JUL-2002 (first entry) XX M12-G4 Y63A mutant of the antithrombotic rattlesnake protein. XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;

KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 XX drug efficacy; mutant; mutein.  
 OS Crotales horridus horridus.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 63 /note="Wild-type Tyr substituted by Ala"  
 PN EPI195384-A1.  
 PD 10-APR-2002.  
 PF 04-OCT-2001; 2001EP-00123277.  
 PR 04-OCT-2000; 2000JP-00305279.  
 PA (AJIN ) AJINOMOTO CO INC.  
 PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,  
 PI Gondoh K, Shimba N, Yamada N;  
 DR WPI; 2002-364482/40.  
 XX Glycoprotein Ib-binding protein, useful for creating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.  
 PS Example 4; Page; 49pp; English.  
 XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC Y63A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 CC protein of the invention. NOTE: This mutant protein sequence is not shown  
 CC in the specification. It has been created from information provided in  
 CC Example 4  
 SQ Sequence 126 AA;  
 XX  
 SQ  
 Query Match 97.1%; Score 675; DB 5; Length 126;  
 Best Local Similarity 97.6%; Pred. No. 1.6e-70;  
 Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DLECPSGMSSTRYCYKPFKQEMTWASAEFPCSEQAKGHLISVETALASFDVNLVYAN 60  
 DB 1 DLECPSGMSSTRYCYKPFKQEMTWADAEFPCSEQAKGHLISVETALASFDVNLVYAN 60  
 QY 61 KEVLTIRYIWIGLRVQNGKQPCSSISYENLVDPCECFMVSRTLRERFVDCQOHSFIC 120  
 DB 61 KEVLTIRYIWIGLRVQNGKQPCSSISYENLVDPCECFMVSRTLRERFVDCQOHSFIC 120  
 QY 121 KFTTRPR 126  
 DB 121 KFTTRPR 126  
 RESULT 19  
 AAO20987  
 ID AAO20987 standard; protein; 126 AA.  
 AC AAO20987;  
 DT 19-JUL-2002 (first entry)  
 DE M14-G4 Y67A mutant of the antithrombotic rattlesnake protein.  
 XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy; mutant; mutein.

XX Crotales horridus horridus.  
 OS Synthetic.  
 OS Crotales horridus horridus.  
 FH Key Location/Qualifiers  
 FT Misc-difference 67 /note="Wild-type Tyr substituted by Ala"  
 PN EPI195384-A1.  
 PD 10-APR-2002.  
 PF 04-OCT-2001; 2001EP-00123277.  
 PR 04-OCT-2000; 2000JP-00305279.  
 PA (AJIN ) AJINOMOTO CO INC.  
 PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,  
 PI Gondoh K, Shimba N, Yamada N;  
 DR WPI; 2002-364482/40.  
 XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
 PT comprises specific mutations in protein originating from snake venom.  
 PS Example 4; Page; 49pp; English.  
 XX The invention relates to a glycoprotein Ib-binding protein, originating  
 CC from snake venom, comprising specific mutations and antithrombotic  
 CC activity. Glycoprotein Ib-binding protein is used in a drug having  
 CC antithrombotic activity. Glycoprotein Ib-binding protein has a high  
 CC binding activity to glycoprotein Ib, a long half life/drug efficacy  
 CC retention in blood, and low antigenicity. This sequence represents the  
 CC Y67A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
 CC protein of the invention. NOTE: This mutant protein sequence is not shown  
 CC in the specification. It has been created from information provided in  
 CC Example 4  
 SQ Sequence 126 AA;  
 XX  
 SQ  
 Query Match 97.1%; Score 675; DB 5; Length 126;  
 Best Local Similarity 97.6%; Pred. No. 1.6e-70;  
 Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DLECPSGMSSTRYCYKPFKQEMTWASAEFPCSEQAKGHLISVETALASFDVNLVYAN 60  
 DB 1 DLECPSGMSSTRYCYKPFKQEMTWADAEFPCSEQAKGHLISVETALASFDVNLVYAN 60  
 QY 61 KEVLTIRYIWIGLRVQNGKQPCSSISYENLVDPCECFMVSRTLRERFVDCQOHSFIC 120  
 DB 61 KEVLTIRYIWIGLRVQNGKQPCSSISYENLVDPCECFMVSRTLRERFVDCQOHSFIC 120  
 QY 121 KFTTRPR 126  
 DB 121 KFTTRPR 126  
 RESULT 20  
 AAO20982  
 ID AAO20982 standard; protein; 126 AA.  
 AC AAO20982;  
 DT 19-JUL-2002 (first entry)  
 DE M9-G4 Y58A mutant of the antithrombotic rattlesnake protein.  
 XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
 KM antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
 KM drug efficacy; mutant; mutein.  
 OS Crotales horridus horridus.



OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 58 /note= "Wild-type Tyr substituted by Ala"  
FT  
XX  
XX EPI195384-A1.  
XX  
XX 10-APR-2002.  
XX  
XX 04-OCT-2001; 2001EP-00123277.  
XX  
XX 04-OCT-2000; 2000JP-00305279.  
XX  
XX (AJIN ) AJINOMOTO CO INC.  
XX  
XX Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
XX Gondoh K, Shinda N, Yamada N;  
XX WPI; 2002-364482/40.  
XX  
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
XX comprises specific mutations in protein originating from snake venom.  
XX  
XX Example 4; Page; 49pp; English.  
XX  
XX The invention relates to a glycoprotein Ib-binding protein, originating  
XX from snake venom, comprising specific mutations and antithrombotic  
XX activity. Glycoprotein Ib-binding protein is used in a drug having  
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high  
XX binding activity to glycoprotein Ib, a long half life/drug efficacy  
XX retention in blood, and low antigenicity. This sequence represents the  
XX Y58A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake  
XX CC protein of the invention. NOTE: This mutant protein sequence is not shown  
XX in the specification. It has been created from information provided in  
XX Example 4  
XX  
XX Sequence 126 AA;  
SQ

Query Match 97.1%; Score 675; DB 5; Length 126;  
Best Local Similarity 97.6%; Pred. No. 1.6e-70;  
Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPKQKEMTWASAEKFCSEQAKGHLISVETALBASFYDNLVYAN 60  
DB 1 DLECPGMSSTDRYCYKPKQKEMTWADAEKFCSEQAKGHLISVETALBASFYDNLVYAN 60  
QY 61 KEYLTRYIWIIGLRVQNKQPCSSISYENLVDPPECFMVSRDTRLREMFKVDCEQHSFIC 120  
DB 61 KEYLTRYIWIIGLRVQNKQPCSSISYENLVDPPECFMVSRDTRLREMFKVDCEQHSFIC 120  
QY 121 KFTRR 126  
DB 121 KFTRR 126

RESULT 21  
AAO20998  
ID AAO20998 standard; protein, 126 AA.  
XX  
XX AAO20998;  
XX  
XX 19-JUL-2002 (first entry)  
XX  
XX M25-G4 D101A, E106Q mutant of antithrombotic rattlesnake protein.  
XX  
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
XX antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
XX drug efficacy; mutant; mutein.  
XX  
XX Crotalus horridus horridus.  
XX Synthetic.  
XX

FH Key Location/Qualifiers  
FT Misc-difference 101 /note= "Wild-type Asp substituted by Ala"  
FT  
XX  
XX Misc-difference 106 /note= "Wild-type Glu substituted by Gln"  
XX  
XX EPI195384-A1.  
XX  
XX 10-APR-2002.  
XX  
XX 04-OCT-2001; 2001EP-00123277.  
XX  
XX 04-OCT-2000; 2000JP-00305279.  
XX  
XX (AJIN ) AJINOMOTO CO INC.  
XX  
XX Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;  
XX Gondoh K, Shinda N, Yamada N;  
XX WPI; 2002-364482/40.  
XX  
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
XX comprises specific mutations in protein originating from snake venom.  
XX  
XX Example 6; Page; 49pp; English.  
XX  
XX The invention relates to a glycoprotein Ib-binding protein, originating  
XX from snake venom, comprising specific mutations and antithrombotic  
XX activity. Glycoprotein Ib-binding protein is used in a drug having  
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high  
XX binding activity to glycoprotein Ib, a long half life/drug efficacy  
XX retention in blood, and low antigenicity. This sequence represents the  
XX D101A, E106Q mutant of the antithrombotic AS1051 126-mer wild-type  
XX CC rattlesnake protein of the invention. NOTE: This mutant protein sequence  
XX is not shown in the specification. It has been created from information  
XX provided in Example 6  
XX  
XX Sequence 126 AA;  
SQ

Query Match 96.8%; Score 673; DB 5; Length 126;  
Best Local Similarity 96.8%; Pred. No. 2.8e-70;  
Matches 122; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPKQKEMTWASAEKFCSEQAKGHLISVETALBASFYDNLVYAN 60  
DB 1 DLECPGMSSTDRYCYKPKQKEMTWADAEKFCSEQAKGHLISVETALBASFYDNLVYAN 60  
QY 61 KEYLTRYIWIIGLRVQNKQPCSSISYENLVDPPECFMVSRDTRLREMFKVDCEQHSFIC 120  
DB 61 KEYLTRYIWIIGLRVQNKQPCSSISYENLVDPPECFMVSRDTRLREMFKVDCEQHSFIC 120  
QY 121 KFTRR 126  
DB 121 KFTRR 126

RESULT 22  
AAO20996  
ID AAO20996 standard; protein, 126 AA.  
XX  
XX AAO20996;  
XX  
XX 19-JUL-2002 (first entry)  
XX  
XX M23-G4 D54N, D101A mutant of antithrombotic rattlesnake protein.  
XX  
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;  
XX antithrombotic; glycoprotein Ib; long half life; low antigenicity;  
XX drug efficacy; mutant; mutein.  
XX  
XX Crotalus horridus horridus.  
XX Synthetic.  
XX

Key	Location/Qualifiers
FT	Misc-difference 54 /note= "Wild-type Asp substituted by Asn"
FT	Misc-difference 101 /note= "Wild-type Asp substituted by Ala"
FT	Misc-difference 101 /note= "Wild-type Asp substituted by Ala"
PN	EP1195384-A1.
XX	10-APR-2002.
PD	04-OCT-2001; 2001EP-00123277.
XX	04-OCT-2001; 2000JP-00305279.
XX	(AJIN ) AJINOMOTO CO INC.
PA	Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI	Gondoh K, Shimba N, Yamada N;
XX	WPI, 2002-364482/40.
DR	Example 6; Page; 49pp; English.
XX	The invention relates to a glycoprotein Ib-binding protein, originating
CC	from snake venom, comprising specific mutations and antithrombotic
CC	activity. Glycoprotein Ib-binding protein is used in a drug having
CC	antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC	binding activity to glycoprotein Ib, a long half life/drug efficacy
CC	retention in blood, and low antigenicity. This sequence represents the
CC	D54N, D101A mutant of the antithrombotic AS1051 126-mer wild-type
CC	rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC	is not shown in the specification. It has been created from information
CC	provided in Example 6
XX	Sequence 126 AA;
XX	50
Query Match	96.5%; Score 671; DB 5; Length 126;
Best Local Similarity	96.8%; Pred. No. 4.8e-70;
Matches 122; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
QY	1 DLECGSGMSSTDYRYKPKPKQMTWASAEKFCSEQAKGHLISVETALASFDVNVLYAN 60
DB	1 DLECPGMSSTYRYCYKPKPKQMTWADAEKFCSEQAKGHLISVETALASFDVNVLYAN 60
QY	61 KEYLRYRWIGLRVGNKQPCSSISYENLVDPFECFMTSPDRRLREWKVDCQOHSFTC 120
DB	61 KEYLRYRWIGLRVGNKQPCSSISYENLVDPFECFMTSPDRRLREWKVDCQOHSFTC 120
QY	121 KFTRRP 126
DB	121 KFTRRP 126
RESULT 23	
ID	AAO20999 standard; protein; 126 AA.
XX	AAO20999;
XX	19-JUL-2002 (first entry)
DE	M26-G4 D101A, E106A mutant of antithrombotic rattlesnake protein.
XX	Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW	antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW	drug efficacy; mutant; mutein.
XX	Crotalus horridus horridus.
OS	Synthetic.
XX	

Key	Location/Qualifiers
PH	Misc-difference 101
FT	/note= "Wild-type Asp substituted by Ala"
FT	Misc-difference 106
FT	/note= "Wild-type Glu substituted by Ala"
XX	
PN	EP1195384-Al.
XX	
PD	10-APR-2002.
XX	
PF	04-OCT-2001; 2001EP-00123277.
XX	
PR	04-OCT-2000; 2000JP-00305279.
XX	
PA	(AJIN ) AJINOMOTO CO INC.
XX	
PI	Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,
PI	Gondoh K, Shimba N, Yamada N;
XX	
DR	WPI; 2002-364482/40.
XX	
PT	Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT	comprises specific mutations in protein originating from snake venom.
XX	
PS	Example 6; Page; 49pp; English.
XX	
CC	The invention relates to a glycoprotein Ib-binding protein, originating
CC	from snake venom, comprising specific mutations and antithrombotic
CC	activity. Glycoprotein Ib-binding protein is used in a drug having
CC	antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC	binding activity to glycoprotein Ib, a long half life/drug efficacy
CC	retention in blood, and low antigenicity. This sequence represents the
CC	D101A, E106A mutant of the antithrombotic AS1051 126-mer wild-type
CC	rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC	is not shown in the specification. It has been created from information
CC	provided in Example 6
XX	
SQ	Sequence 126 AA:
XX	
Query Match	96.4%; Score 670; DB 5; Length 126;
Best Local Similarity	96.8%; Pred. No. 6.3e-70;
Matches 122; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	1 DLEPCSGMSIDRYCYCPKQEMTWAGAEFCSEQAGGHLISVETALIASFVNNVLYAN 60
DB	1 DLEPCSGMSYDRXCYPFKQEMTWADAEFCSEQAGGHLISVETALIASFVNNVLYAN 60
QY	61 KEYLTRYTWIGLARVONKGPCCSSISYENLVDPFECFVWSRPTRLREMKVDCQOHSFIC 120
DB	61 KEYLTRYTWIGLARVONKGPCCSSISYENLVDPFECFVWSRATRLRAMEKVDCEQOHSFIC 120
QY	121 KFTRRP 126
DB	121 KFTRRP 126
XX	
RESULT 24	
ID	AAO20997 standard; protein; 126 AA.
XX	
AC	AAO20997;
XX	
DT	19-JUL-2002 (first entry)
XX	
DE	M2A-G4 D5A, D101A mutant of antithrombotic rattlesnake protein.
XX	
KW	Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW	antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW	drug efficacy; mutant; mutein.
XX	
OS	Crotalus horridus horridus.
OS	Synthetic.
XX	

```

FH Key Location/Qualifiers
FT Misc-difference 54 /note= "Wild-type Asp substituted by Ala"
FT FT Misc-difference 101 /note= "Wild-type Asp substituted by Ala"
PN EP1195384-Al.
XX
XX 10-APR-2002.
PD
XX 04-OCT-2001; 2001EP-00123277.
XX
XX 04-OCT-2000; 2000JP-00305279.
XX
XX (AJIN ) AJINOMOTO CO INC.
PA
XX Fukuichi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
XX WPI: 2002-364482/40.
DR
XX
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
XX Example 6; Page; 49pp; English.
PS
XX
XX The invention relates to a glycoprotein Ib-binding protein, originating
CC from snake venom, comprising specific mutations and antithrombotic
CC activity. Glycoprotein Ib-binding protein is used in a drug having
CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC binding activity to glycoprotein Ib, a long half life/drug efficacy
CC retention in blood, and low antigenicity. This sequence represents the
CC D54A, D101A mutant of the antithrombotic AS1051 126-mer wild-type
CC rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC is not shown in the specification. It has been created from information
XX provided in Example 6
XX
SQ Sequence 126 AA;
Query Match 96.1%; Score 668; DB 5; Length 126;
Best Local Similarity 96.8%; Pred. No. 1,1e-69;
Matches 122; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 DLECPGSGMSIDRYCYKPKFQKQMTWASAEKFCSEQAKGHLISVETALASFDVNVLYAN 60
DB 1 DLECPGSGMSYDRYCYKPKFQKQMTWADAEKFCSEQAKGHLISVETALASFDVNVLYAN 60
QY 61 KEYLTRYTWIGLGRVGNKQPCSSISYENLVNPFECFMSRPRRLAEWKVDCQEQHSFTC 120
DB 61 KEYLTRYTWIGLGRVGNKQPCSSISYENLVNPFECFMSRPRRLAEWKVDCQEQHSFTC 120
QY 121 KETRRP 126
DB 121 KETRRP 126
RESULT 25
AAO20994
ID AAO20994 standard; protein; 126 AA.
XX
XX AAO20994;
XX
XX 19-JUL-2002 (first entry)
DE M21-G4 D54A, D101N, E106Q mutant of antithrombotic rattlesnake protein.
XX
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy; mutant; mutein.
XX
XX Crocatus horridus horridus.
XX
XX Synthetic.
XX

```

Key	Location/Qualifiers
PH	Misc-difference 54
FT	/note= "wild-type Asp substituted by Ala"
FT	Misc-difference 101
FT	/note= "wild-type Asp substituted by Asn"
FT	Misc-difference 106
FT	/note= "wild-type Glu substituted by Gln"
XX	
FN	EP1195384-A1.
XX	
PD	10-APR-2002.
XX	
PE	04-OCT-2001; 2001EP-00123277.
XX	
PR	04-OCT-2000; 2000JP-00305279.
XX	
PA	(AJIN ) AJINOMOTO CO INC.
PI	Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI	Gordon K, Shimba N, Yamada N;
XX	
XX	WPI; 2002-364482/40.
XX	
PT	Glycoprotein Ib-binding protein, useful for treating thrombosis.
PT	comprises specific mutations in protein originating from snake venom.
XX	
PS	Example 6; Page; 49pp; English.
XX	
CC	The invention relates to a glycoprotein Ib-binding protein, originating
CC	from snake venom, comprising specific mutations and antithrombotic
CC	activity. Glycoprotein Ib-binding protein is used in a drug having
CC	antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC	binding activity to glycoprotein Ib, a long half life/drug efficacy
CC	reversion in blood, and low antigenicity. This sequence represents the
CC	D54A, D101N, E106Q mutant of the antithrombotic ASI051 126-mer wild-type
CC	rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC	is not shown in the specification. It has been created from information
CC	provided in Example 6
XX	
SQ	Sequence 126 AA;
XX	
Query Match	96.1%; Score 668; DB 5; Length 126;
Best Local Similarity	96.0%; Pred. No. 1,1e-69;
Matches 121; Conservative 2; Mismatches 3; Indels 0; Gaps 0	
Qy	1 DLECPGSGSSDRVCYKPFKQEMTWASERFCSEQAKGHLISVETALEASFVDNVLAYAN 60
Db	1 DLECPGSGSSDRVCYKPFKQEMTWADDERFCSEQAKGHLISVETALEASFVNVLYAN 60
Qy	61 KEYLTRYIWMIGLRVONKQPCSSISYENLVDPFCFMYVSRDTRLREMKVDCQEQHSFIC 120
Db	61 KEYLTRYIWMIGLRVONKQPCSSISYENLVDPFCFMYVSRTRLRQMKVDCQEQHSFIC 120
Qy	121 KFTPRR 126
Db	121 KFTPRR 126
XX	
RESULT 26	
AAO20995	AAO20995 standard; protein, 126 AA.
XX	
AAO20995;	
XX	
DT	19-JUL-2002 (first entry)
XX	
DE	M22-G4 D54A, D101A, E106A mutant of antithrombotic rattlesnake protein.
XX	
KW	Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW	antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW	drug efficacy; mutant; mutain.
XX	
DS	Crotalus horridus horridus.

```

OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 54
FT /note= "Wild-type Asp substituted by Ala"
FT Misc-difference 101
FT /note= "Wild-type Asp substituted by Ala"
FT Misc-difference 106
FT /note= "Wild-type Glu substituted by Ala"
XX
XX EP1195384-A1.
XX
XX 10-APR-2002.
XX
XX 04-OCT-2001; 2001EP-00123277.
XX
XX 04-OCT-2000; 2000JP-00305279.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Fukuchi N, Kato M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
XX Gondo K, Shiba N, Yamada N;
XX
XX WPI; 2002-364482/40.
XX
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,
XX comprises specific mutations in protein originating from snake venom.
XX
XX Example 6; Page; 49pp; English.
XX
XX The invention relates to a glycoprotein Ib-binding protein, originating
XX from snake venom, comprising specific mutations and antithrombotic
XX activity. Glycoprotein Ib-binding protein is used in a drug having
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high
XX binding activity to glycoprotein Ib, a long half life/drug efficacy
XX retention in blood, and low antigenicity. This sequence represents the
XX D54A, D101A, E106A mutant of the antithrombotic AS1051 126-mer wild-type
XX rattlesnake protein of the invention. NOTE: This mutant protein sequence
XX is not shown in the specification. It has been created from information
XX provided in Example 6
XX
XX Sequence 126 AA;
XX
Query Match 95.3%; Score 662; DB 5; Length 126;
Best Local Similarity 96.0%; Pred. No. 5.5e-69;
Matches 121; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 DLECPGMSSTDRYCYKPKQEMTWASARFCSEQAKGHLISVETALASFPVDNVLNAN 60
DB 1 DLECPGMSSTDRYCYKPKQEMTWADARFCSEQAKGHLISVETALASFPVAVNLNAN 60
QY 61 KEYLIRYIWIGLRVQNKQPCSSISYENLVDPFECFMSRDTLRLEWFKVDCQCHSFTC 120
DB 61 KEYLIRYIWIGLRVQNKQPCSSISYENLVDPFECFMSRDTLRLEWFKVDCQCHSFTC 120
QY 121 KFTRRP 126
DB 121 KFTRRP 126
XX
RESULT 27
AAR24426
ID AAR24426 standard; protein; 127 AA.
XX
XX AAR24426;
XX
XX 25-MAR-2003 (revised)
XX 21-NOV-1992 (first entry)
XX
XX Sequence of the platelet glycoprotein GPIb inhibitor alpha chain (CHH-B-
XX alpha).
XX Platelet adherence inhibitor; platelet anti-adhesive;

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KW antithrombotic agent; von Willebrand factor;
KW platelet glycoprotein GPIb-IX complex.
XX
XX Crocetalus horridus horridus.
XX
XX WO9208472-A1.
XX
XX 29-MAY-1992.
XX
XX 14-NOV-1991; 91WO-US0008516.
XX
XX 16-NOV-1990; 90US-00614443.
XX
XX (CORF-) COR THERAPEUTICS INC.
XX
XX Scarborough RM;
XX
XX WPI; 1992-19936/24.
XX
XX Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit
XX thrombus formation; for treatment of arteriosclerosis, atherosclerosis,
XX acute myocardial infarction, chronic unstable angina, etc.
XX
XX Example; Fig 6; 5pp; English.
XX
XX The PAA was purified from a solution of snake venom. Analysis of the peak
XX inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with
XX a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin
XX induced platelet agglutination. They were called CHH-A and CHH-B. The
XX earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-
XX alpha) were individually submitted to N-terminal sequence analysis. The
XX complete amino acid sequence for the alpha and beta chains are given in
XX AAR24426 and AAR24427. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 127 AA;
XX
Query Match 95.1%; Score 661; DB 2; Length 127;
Best Local Similarity 96.0%; Pred. No. 7.2e-69;
Matches 121; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 DLECPGMSSTDRYCYKPKQEMTWASARFCSEQAKGHLISVETALASFPVDNVLNAN 60
DB 1 DLECPGMSSTDRYCYKPKQEMTWADARFCSEQAKGHLISVETALASFPVAVNLNAN 60
QY 61 KEYLIRYIWIGLRVQNKQPCSSISYENLVDPFECFMSRDTLRLEWFKVDCQCHSFTC 120
DB 61 KEYLIRYIWIGLRVQNKQPCSSISYENLVDPFECFMSRDTLRLEWFKVDCQCHSFTC 120
QY 121 KFTRRP 126
DB 121 KFTRRP 126
XX
RESULT 28
AAO20975
ID AAO20975 standard; protein; 110 AA.
XX
XX AAO20975;
XX
XX 19-JUL-2002 (first entry)
XX
XX 110-mer central loop-deficient rattlesnake protein.
XX
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
XX antithrombotic; glycoprotein Ib; long half life; low antigenicity;
XX drug efficacy; loop-deficient.
XX
XX Crocetalus horridus horridus.
XX
XX Synthetic.
XX
XX EP1195384-A1.
XX
XX 10-APR-2002.

```

XX 04-OCT-2001; 2001EP-00123277.  
XX  
XX 04-OCT-2000; 2000JP-00305279.  
XX  
XX (AJIN) AJINOMOTO CO INC.  
XX  
XX Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E,  
XX Gondoh K, Shinya N, Yamada N;  
XX WPI; 2002-36482/40.  
XX  
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,  
XX comprises specific mutations in protein originating from snake venom.  
XX  
XX Example 2; Page 28; 49pp; English.  
XX  
XX The invention relates to a glycoprotein Ib-binding protein, originating  
XX from snake venom, comprising specific mutations and antithrombotic  
XX activity. Glycoprotein Ib-binding protein is used in a drug having  
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high  
XX binding activity to glycoprotein Ib, a long half life/drug efficacy  
XX retention in blood, and low antigenicity. This sequence represents the  
XX 110-mer central loop-deficient rattlesnake protein relating to the  
XX invention  
XX  
XX Sequence 110 AA:  
SQ  
Query Match 79.3%; Score 551; DB 5; Length 110;  
Best Local Similarity 82.5%; Pred. No. 4.3e-56;  
Matches 104; Conservative 0; Mismatches 6; Indels 16; Gaps 1;  
QY 1 DLECPGMSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLSEVETALASFPVDNVLVAN 60  
DB 1 DLECPGMSSTDRYCYKPFKQEMTWADAEKFCSEQAKGHLSEVETALASFPVDNVLVAN 60  
QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYENLVDPCEFWNSRDTLRERFKYDCEQHSFIC 120  
DB 61 KEYLTRYIWIIGLRGCG-----ECFVNSRDTLRERFKYDCEQHSFIC 104  
QY 121 KFTRR 126  
DB 105 KFTRR 110  
RESULT 29  
AAE20181  
ID AAE20181 standard; protein; 158 AA.  
XX  
XX AAE20181;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Pigmy rattlesnake venom gland protein, Zank5.  
XX  
XX Pigmy rattlesnake; venom gland protein, blood coagulation; therapy;  
XX platelet aggregation; Zank5.  
XX  
XX Sistrurus miliaris.  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..23  
XX Protein 24..158  
XX Disulfide-bond 27..38 /label= Mature\_Zank5\_protein  
XX Disulfide-bond 55..152  
XX Disulfide-bond 127..144  
XX  
XX WO200214364-A2.  
XX  
XX 21-FEB-2002.  
XX

PF 13-AUG-2001; 2001WO-US025310.  
XX  
XX 14-AUG-2000; 2000US-0225072P.  
XX  
XX 14-AUG-2000; 2000US-0225087P.  
XX  
XX 15-AUG-2000; 2000US-0225489P.  
XX  
XX 15-AUG-2000; 2000US-0225490P.  
XX  
XX 20-DEC-2000; 2000US-0256997P.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
XX Sheppard PO, Bishop PD;  
XX  
XX WPI; 2002-269180/31.  
XX  
XX N-PSDB; AAD32059.  
XX  
XX New pigmy rattlesnake (Sistrurus miliaris) venom gland protein, which  
XX affect blood coagulation and platelet aggregation system, useful in  
XX therapy and diagnostics, or as tools in the study of genetics or  
XX molecular biology.  
XX  
XX Claim 3; Page 3; 79pp; English.  
XX  
XX The invention relates to new pigmy rattlesnake (Sistrurus miliaris)  
XX venom gland proteins, which affect blood coagulation and platelet  
XX aggregation system. The polypeptides, which affect blood coagulation and  
XX platelet aggregation system, are useful in therapy and diagnostics. The  
XX polypeptides are also useful as an educational tool in laboratory  
XX practical kits for courses related to genetics and molecular biology,  
XX protein chemistry and antibody production and analysis. The  
XX polynucleotide or polypeptide can be used as standards or as unknowns for  
XX testing purposes. The polypeptides are also useful in identifying  
XX proteins by western blotting, protein purification, determining the  
XX weight of expressed polypeptides as a ratio to total protein expressed,  
XX identifying peptide cleavage sites, coupling amino and carboxyl terminal  
XX tags, mass spectrometry, circular dichroism to determine conformation or  
XX affinity chromatography columns to purify the protein, cloning or  
XX sequencing. The present sequence is Sistrurus miliaris venom gland  
XX protein, Zank5  
XX  
XX Sequence 158 AA:  
SQ  
Query Match 52.0%; Score 361.5; DB 5; Length 158;  
Best Local Similarity 50.4%; Pred. No. 9.6e-34;  
Matches 66; Conservative 21; Mismatches 35; Indels 9; Gaps 2;  
QY 1 DLECPGMSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLSEVETALASFPVDNVLVAN 60  
DB 24 DLECPGMSSTDRYCYKPFKQEMTWADAEKFCSEQAKGHLSEVETALASFPVDNVLVAN 83  
QY 61 KEYLTRYIWIIGLRVONKQGPC-----SSISYENLVDPF--ECFVNSRDTLRERFKYD 111  
DB 84 IKONQYIWIIGLRVONKQGPCSTKMSDSSVSISYENLVSHSKKCFGLKRETEPLQWNTD 143  
QY 112 CEQHSFICKF 122  
DB 144 CEKNUFVCKF 154  
RESULT 30  
AAR38228  
ID AAR38228 standard; protein; 130 AA.  
XX  
XX AAR38228;  
XX  
XX 25-MAR-2003 (revised)  
XX  
XX 01-OCT-1993 (first entry)  
XX  
XX Sequence of polypeptide chain of alboaegregin B1 (AL-B2).  
XX  
XX Venom; snake; platelet-binding protein.  
XX  
XX Trimeresurus albolabris.  
XX

```
PN WO9311151-A1.
XX
XX 10-JUN-1993.
XX
XX 01-DEC-1992; 92WO-US010344.
XX
XX 03-DEC-1991; 91US-00803630.
XX
XX 05-JUN-1992; 92US-00893929.
XX
XX (UTEM ) UNIV TEMPLE.
XX
XX Kirby EP, Peng M;
XX
XX WPI; 1993-196991/24.
XX
XX New platelet-binding proteins obtained from snake venom - inhibit binding
XX of von Willebrand factor to platelet membrane glycoprotein IB, useful in
XX therapy, diagnosis and surgery.
XX
XX Claim 8; Page 48; 74pp; English.
XX
XX Alboagregin B1 and B2 (collectively "Al-B"), may be obtained in
XX substantially pure chemical form from venom. Each of Al-B1 and -B2
XX comprise an about 23 kDa protein formed by an about 17 kDa polypeptide
XX chain crosslinked to an about 14 kDa polypeptide chain by one or more
XX interchain disulfide bonds. Each of the two polypeptide chains of Al-B1
XX and -B2 show strong homology to two of the chains of Al-A. Al-B1 and -B2
XX each comprise two non-identical polypeptide chains. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 130 AA;
SQ
Query Match 49.0%; Score 340.5; DB 2; Length 130;
Best Local Similarity 50.8%; Pred. No. 2,1e-31;
Matches 66; Conservative 22; Mismatches 29; Indels 13; Gaps 4;
QY 3 ECPSGWSTDRYCYKPFKQEMTWSAARFCSEQAKGHLISVETALASFDVNDVLYANKE 61
DB 1 DCPSDWSSFKQYCYQIVALKETWEDAEKFCSEQANDGHVLSIESREAVFVALLSENK 60
QY 62 EYLTRYIWIIGLRVONKGQPC-----SSISYENLV--DPFECFMYSRDTRLREMFKVDCE 112
DB 61 KY--HWMIIGLSVONKQCCSEWSDSSVSYENLVKPKCFVLKKESEFRTWSNVYCE 117
QY 113 EQQHSFICKF 122
DB 118 EOKHIFMCKF 127
QY
DB
RESULT 31
AAR38226
ID AAR38226 standard; protein; 132 AA.
XX
XX AAR38226;
XX
XX 25-MAR-2003 (revised)
XX
XX 01-OCT-1993 (first entry)
XX
XX Sequence of polypeptide chain of alboagregin B1 (Al-B1).
XX
XX Venom; snake; platelet-binding protein.
XX
XX Trimeresurus albolabris.
XX
XX WO9311151-A1.
XX
XX 10-JUN-1993.
XX
XX 01-DEC-1992; 92WO-US010344.
XX
XX 03-DEC-1991; 91US-00803630.
XX
XX 05-JUN-1992; 92US-00893929.
XX
```

```
PA (UTEM ) UNIV TEMPLE.
XX
XX Kirby EP, Peng M;
XX
XX WPI; 1993-196991/24.
XX
XX New platelet-binding proteins obtained from snake venom - inhibit binding
XX of von Willebrand factor to platelet membrane glycoprotein IB, useful in
XX therapy, diagnosis and surgery.
XX
XX Claim 6; Page 47; 74pp; English.
XX
XX Alboagregin B1 and B2 (collectively "Al-B"), may be obtained in
XX substantially pure chemical form from venom. Each of Al-B1 and -B2
XX comprise an about 23 kDa protein formed by an about 17 kDa polypeptide
XX chain crosslinked to an about 14 kDa polypeptide chain by one or more
XX interchain disulfide bonds. Each of the two polypeptide chains of Al-B1
XX and -B2 show strong homology to two of the chains of Al-A. Al-B1 and -B2
XX each comprise two non-identical polypeptide chains. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 132 AA;
SQ
Query Match 46.4%; Score 322.5; DB 2; Length 132;
Best Local Similarity 47.3%; Pred. No. 2,7e-29;
Matches 61; Conservative 21; Mismatches 38; Indels 9; Gaps 2;
QY 3 ECPSGWSTDRYCYKPFKQEMTWSAARFCSEQAKGHLISVETALASFDVNDVLYANKE 62
DB 1 DCPSDWSSFKQYCYQIVALKETWEDAEKFCSEQANDGHVLSIESREAVFVALLSENK 60
QY 63 YLTRYIWIIGLRVONKGQPC-----SSISYENLV--DPFECFMYSRDTRLREMFKVDCE 113
DB 61 TTKYVWMIIGLSVONKQCCSEWSDSSVSYENLVKPKCFVLKKESEFRTWSNVYCE 120
QY 114 EQQHSFICKF 122
DB 121 EOKHIFMCKF 129
QY
DB
RESULT 32
AAR38222
ID AAR38222 standard; protein; 131 AA.
XX
XX AAR38222;
XX
XX 25-MAR-2003 (revised)
XX
XX 01-OCT-1993 (first entry)
XX
XX Sequence of polypeptide chain of alboagregin A (Al-A).
XX
XX Venom; snake; platelet-binding protein.
XX
XX Trimeresurus albolabris.
XX
XX WO9311151-A1.
XX
XX 10-JUN-1993.
XX
XX 01-DEC-1992; 92WO-US010344.
XX
XX 03-DEC-1991; 91US-00803630.
XX
XX 05-JUN-1992; 92US-00893929.
XX
XX (UTEM ) UNIV TEMPLE.
XX
XX Kirby EP, Peng M;
XX
XX WPI; 1993-196991/24.
XX
XX New platelet-binding proteins obtained from snake venom - inhibit binding
XX of von Willebrand factor to platelet membrane glycoprotein IB, useful in
XX therapy, diagnosis and surgery.
XX
```







DR WPI; 1993-196991/24.  
 XX New platelet-binding proteins obtained from snake venom - inhibit binding  
 PT of von Willebrand factor to platelet membrane glycoprotein IB, useful in  
 PT therapy, diagnosis and surgery.  
 XX  
 PS Claim 4; Page 46; 74pp; English.  
 CC AL-A may be obtcd. from snake venom. It has a mol. wt. of about 45 kDa. AL  
 CC -A contains two types of polypeptide chains, with mol. wt. of about 18  
 CC kDa and about 15 kDa, respectively. Each of these two types of chains is  
 CC actually composed of two subtypes. Thus, AL-A comprises four non-  
 CC identical polypeptide chains. A possible variation of AAR38224 has been  
 CC found, characterised by Asp at posn. three in lieu of Cys. (Updated on 25  
 CC MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 134 AA;  
 SO  
 Query Match 44.2%; Score 307.5; DB 2; Length 134;  
 Best Local Similarity 42.0%; Pred. No. 1.6e-27;  
 Matches 55; Conservative 26; Mismatches 41; Indels 9; Gaps 2;  
 QY 1 DLECPGMSSTDRYCYKPKQEMTWASAEKFCSEQAKGHLISVETRLAESFVDNLYAN 60  
 DB 1 DFCFLGMSAYDQCYRVFNEPKWEDAEKFCQAKDQSGHLVSIETGSEADFVAOLISEN 60  
 QY 61 KEVLTFTYIMIGLRVONKGGPC-----SSISYENLVDPF--CFMWSRDLRLREMFKYD 111  
 DB 61 IQCKEYHVMIGLWVONKEQCSSEMSDGSSTYENLTKLTKMRKGALEQSGFRKMINUG 120  
 QY 112 CEQOHSFICK 122  
 DB 121 CIGLNPFVCKF 131  
 RESULT 37  
 AAO14520  
 ID AAO14520 standard; protein; 154 AA.  
 XX  
 AC AAO14520;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Korean adder snake venom salmorin A chain protein.  
 XX  
 KW Korean adder; salmorin protein A chain; snake venom;  
 KW fibrinogen clotting inhibition; thrombosis; prothrombin binding;  
 KW thrombin binding; blood coagulation.  
 XX  
 OS Gloydius halys brevicaudus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= signal\_peptide  
 FT Protein 24..154  
 FT /note= "Mature salmorin A chain protein"  
 XX  
 PN W0200214514-A1.  
 PD 21-FEB-2002.  
 XX  
 PF 26-JUL-2001; 2001MO-KR001277.  
 XX  
 PR 27-JUL-2000; 2000KR-00043470.  
 XX  
 PA (BIOB-) BIOBUD CO LTD.  
 XX  
 PI Chung K, Kim D, Koh Y;  
 XX  
 DR WPI; 2002-241907/29.  
 DR N-PSDB; AAL42015.  
 XX

PT New salmorin protein derived from venom of Korean adder Agkistrodon halys  
 PT brevicaudus, useful for treating thrombosis by repressing fibrinogen  
 PT clotting through repression of activation of prothrombin into thrombin.  
 XX  
 PS Claim 2; Fig 1A; 30pp; English.  
 CC The invention comprises the nucleotide and protein sequences of a  
 CC salmorin protein derived from the venom of Korean adder. Salmorin protein  
 CC is composed of an A chain and a B chain, and has inhibitory activity  
 CC against fibrinogen clotting. The salmorin protein of the invention is  
 CC useful for treating thrombosis, as it represses fibrinogen clotting  
 CC potentially by binding to prothrombin and thrombin so as to delay blood  
 CC coagulation. The present amino acid sequence represents the Korean adder  
 CC salmorin A chain protein. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 154 AA;  
 SO  
 Query Match 43.8%; Score 304.5; DB 5; Length 154;  
 Best Local Similarity 44.6%; Pred. No. 4.3e-27;  
 Matches 58; Conservative 20; Mismatches 43; Indels 9; Gaps 2;  
 QY 1 DLECPGMSSTDRYCYKPKQEMTWASAEKFCSEQAKGHLISVETRLAESFVDNLYAN 60  
 DB 24 DFCFLGMSAYDQCYRVFNEPKWEDAEKFCQAKDQSGHLVSIETGSEADFVAOLISEN 63  
 QY 61 KEVLTFTYIMIGLRVONKGGPC-----SSISYENLVDPF--CFMWSRDLRLREMFKYD 111  
 DB 84 IETSPHVMIGLWVONKEQCSSEMSDGSSTYENLTKLTKMRKGALEQSGFRKMINUG 143  
 QY 112 CEQOHSFICK 121  
 DB 144 CGQRNPFVCE 153  
 RESULT 38  
 AAM51543  
 ID AAM51543 standard; protein; 152 AA.  
 XX  
 AC AAM51543;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 10-JAN-2002 (first entry)  
 XX  
 DE Snake venom blood anticoagulant halysin A chain.  
 XX  
 KW Snake; pit viper; venom; halysin; anticoagulant; thrombogenesis;  
 KW thrombosis.  
 XX  
 OS Gloydius halys.  
 XX  
 PN KR2001049671-A.  
 PD 15-JUN-2001.  
 XX  
 PF 29-JUN-2000; 2000KR-00036591.  
 XX  
 PR 29-JUN-1999; 99KR-00025105.  
 XX  
 PA (BIOB-) BIOBUD CO LTD.  
 XX  
 PI Jang YS, Jung GH, Kim DS, Koo BH, Son YD;  
 XX  
 DR WPI; 2001-637330/73.  
 DR N-PSDB; AAT1876.  
 XX  
 PT Halysin as blood anticoagulation protein separated from snake venom.  
 PS Claim 2; Page 10; 21pp; Korean.  
 CC The invention relates to halysin, a novel protein with very strong blood  
 CC anticoagulation activity. The protein was separated from snake venom of  
 CC Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the



CC angiotrophic thrombosis, cerebral thrombosis, ischaemic, cerebral vascular  
 CC diseases, unstable angina, acute thrombosis, unstable stenocardia,  
 CC thromboangitis obliterans, pulmonary embolism, deep vein thrombosis,  
 CC peripheral arterial occlusion, stroke. It is also useful for treating  
 CC atherosclerosis, oedema and inflammation, cancer and neurodegenerative  
 CC diseases. The present sequence represents the amino acid sequence of the  
 CC Deinagkistrodon acutus antithrombosis enzyme alpha chain

XX Sequence 129 AA;

Query Match 39.1%; Score 271.5; DB 6; Length 129;

Best Local Similarity 41.4%; Pred. No. 2,4e-23;

Matches 53; Conservative 22; Mismatches 44; Indels 9; Gaps 2;

QY 3 ECPGSGSTDRVCYKPFKQEMTWASAEPCSEQAKGHLSTVETALASFDVNLVANKK 62  
 DB 1 DCSSDMSYEGHCYKVFQKSKTWTDAESFCTKQVNGHLVSISSGADPVGQLIAQIK 60  
 QY 63 YLTRYIWIIGLRVONKQGPC-----SSISYENLV--DPECFMVSRDTRLREMFVDC 113  
 DB 61 SAKIHWIGLRQONKEKQCSIEWSDGSSISKENWIEESKCKLGVHETGFHKMENFYCE 120  
 QY 114 QQHSFICK 121  
 DB 121 QQDPFVCE 128

RESULT 41

ABU62534  
 ID ABU62534 standard; protein; 129 AA.

XX ABU62534;

XX 23-OCT-2003 (revised)

DT 23-AUG-2003 (first entry)

XX Snake antithrombosis enzyme A chain.

XX Snake; antithrombosis enzyme; A chain; enzyme; fibrin; blood clot;

KM platelet aggregation; myocardial infarction; restenosis; unstable angina;

KM cerebral thrombosis; cardiac; antitanginal; thrombolytic; anticoagulant;

KM vasoactive.

XX Deinagkistrodon acutus.

XX US2003022350-A1.

PD 30-JAN-2003.

PF 23-AUG-2001; 2001US-00938114.

PR 11-APR-1997; 97US-0043886P.

PR 10-APR-1998; 98US-00058740.

XX (WANG/) WANG.C.

PA (LIBX/) LI B X.

PA (CHEN/) CHENG X.

PA (LIU/) LIU J.

PA (NIU/) NIU L.

PA (HUAN/) HUANG W.

PA (XU2/) XU Z.

PA (LUOD/) LUO D.

PA (KANG/) KANG L.

PA (DING/) DING J.

PA (RONG/) RONG F.

PA (LIUY/) LIU Y.

PA (CHEN/) CHEN H.

XX Wang C, Li BX, Cheng X, Liu J, Niu L, Huang W, Xu Z, Luo D,

PI Kang L, Ding J, Rong F, Liu Y, Chen H;

XX WPI; 2003-492002/46.

PT New antithrombosis enzyme, useful for treating or preventing a thrombosis  
 PT related disease in a mammal e.g. myocardial infarction, restenosis,  
 PT unstable angina or cerebral thrombosis.

XX Claim 14; Page 6-7; 20pp; English.

XX The invention relates to an isolated, purified or recombinant

CC antithrombosis enzyme which hydrolyses fibrin, dissolves blood clots and

CC prevents platelet aggregation. The enzyme is useful for treating or

CC preventing a thrombosis related disease in a mammal, such as myocardial

CC infarction, restenosis, unstable angina or cerebral thrombosis. This

CC sequence represents a snake antithrombosis enzyme A chain. (Updated on 23

CC -OCT-2003 to standardise OS field)

XX Sequence 129 AA;

Query Match 39.1%; Score 271.5; DB 7; Length 129;

Best Local Similarity 41.4%; Pred. No. 2,4e-23;

Matches 53; Conservative 22; Mismatches 44; Indels 9; Gaps 2;

QY 3 ECPGSGSTDRVCYKPFKQEMTWASAEPCSEQAKGHLSTVETALASFDVNLVANKK 62  
 DB 1 DCSSDMSYEGHCYKVFQKSKTWTDAESFCTKQVNGHLVSISSGADPVGQLIAQIK 60  
 QY 63 YLTRYIWIIGLRVONKQGPC-----SSISYENLV--DPECFMVSRDTRLREMFVDC 113  
 DB 61 SAKIHWIGLRQONKEKQCSIEWSDGSSISKENWIEESKCKLGVHETGFHKMENFYCE 120  
 QY 114 QQHSFICK 121  
 DB 121 QQDPFVCE 128

RESULT 42

AAR72235  
 ID AAR72235 standard; peptide; 132 AA.

XX AAR72235;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide.

KM Vipera palestinae; venom; antithrombotic agent; platelet binding;

XX von Willebrand factor.

XX Vipera xanthina.

PN W09509183-A1.

PD 06-APR-1995.

PF 27-SEP-1994; 94WO-JP001583.

PR 28-SEP-1993; 93JP-00241666.

PR 14-JUN-1994; 94JP-00002691.

PR 10-JUN-1994; 94JP-00128518.

XX (AJIN ) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI WPI; 1995-147392/19.

XX Peptide derived from Vipera palestinae venom - inhibits binding of

PT platelets to von Willebrand factor, useful as antithrombotic agent.

XX Claim 5; Page 19; 37pp; Japanese.

XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide compn.

CC comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of





XX	Key	Location/Qualifiers
FT	Peptide	1..23
XX		/note= "Leader peptide"
FT	Protein	24..146
FT		/note= "Mature antithrombosis enzyme beta chain. Residues 24 to 40 specifically claimed in claim 8"
FT	Misc-difference	72
FT		/label= Unknown
FT		/note= "Encoded by NNT"
FT	Misc-difference	72
FT		/label= Unknown
FT		/note= "Encoded by NNN"
FT	Misc-difference	72
FT		/label= Unknown
FT		/note= "Encoded by TNN"
XX		
XX	US6489451-B1.	
XX		
PD	03-DEC-2002.	
XX		
PE	10-APR-1998;	98US-00058740.
XX		
PR	10-APR-1997;	97US-0043886P.
PA	(HEFE-) HEFEI SIU FUNG USTC PHARM CO LTD.	
XX		
XX		
PI	Li BX, Cheng X;	
XX		
DR	WPI; 2003-352116/33.	
XX		
DR	N-PSDB; ABX93674.	
XX		
PT	New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and unstable angina.	
XX		
PT		
XX		
PS	Disclosure; Fig 1; 19pp; English.	
XX		
CC	The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, ischaemic cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thromboangiitis obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents the amino acid sequence of the Deinagkistrodon actus antithrombosis enzyme beta chain	
CC		
XX		
XX	Sequence 146 AA;	

	Query Match	Similarity	Score	DB	Length
Best Local	47	30.3%	210.5	DB 6	146
Matches	47	37.6%	Pred. No. 3,8e-16		
			Mismatches 46	Indels 9	Gaps 5
OY	3	ECPSGMSSTDRKCYCPFKOEMTWASAEKPCSOAQNGHH	LSVERALAEASFVDNLYANK	61	
Db	24	DCPSMSWSEYEGCYRPFDEPKTWAAEKCTOOHQSHLPLTA	VRIVLXXXXGHVDRKL	83	
OY	62	EYLTV----RYTWIGLRVONKQPCSSISYENLVDPPECFMS	RDRTRLREWFYDVEQOHS	117	
Db	84	KLISLIGLKNITWNG--CYWKNMSDGRKLYLKIDRDEQPEC	LVSR-IVNNEMSLMDGTCIS	139	

QY	118	FICKF	122
		1:111	
Db	140	FVCKF	144

RESULT 48  
ABU62539  
ID ABU62539 standard; protein; 146 AA.

AC ABU62539;

DT	23-OCT-2003	(revised)
DT	29-AUG-2003	(first entry)

DE Snake antithrombosis enzyme B chain.

KW Snake; antithrombosis enzyme; B chain, enzyme; fibrin; blood clot;  
KW platelet aggregation; myocardial infarction; restenosis; unstable angina;  
KW cerebral thrombosis; cardiac; antidiagonal; thrombolytic; anticoagulant;  
KW vasotrophic.

05 *Deinagkistrodon acutus*.

	Key	Location/Qualifiers
FH	Misc-difference	72. 75
FT		/note= "Encoded by TNNNNNNNNNT"
FT		

PN US2003022350-A1.

PD 30-JAN-2003 .

PF 23-AUG-2001; 2001US-00938114.

PR 11-APR-1997; 97US-0043886P.  
PR 10-APR-1998; 98US-00058740.

PA (WANG/) WANG C.  
PA (LIBX/) LI B X.  
PA (CHEN/) CHENG X.  
PA (LIU/) LIU J.

PA (HUAN/) HUANG W.  
PA (XUZZ/) XU Z.  
PA (LUOD/) LUO D.  
PA (KANG/) KANG L.  
PA (DING/) DING J.  
PA (RONG/) RONG F.  
PA (LIUY/) LIU Y.  
PA (CHEN/) CHEN H.

ca Wang C, Li BX, Cheng X, Liu J, Niu L, Huang W, Xu Z, Luo D;  
PI Kang L, Ding J, Rong F, Liu Y, Chen H;  
PI  
XX  
WP1: 2003-492002/46.  
DR N-PSDB; ACA63110.

PT New antithrombosis enzyme, useful for treating or preventing a thrombosis  
PT related disease in a mammal e.g. myocardial infarction, restenosis,  
PT unstable angina or cerebral thrombosis.

PS Example 3; Fig 1; 20pp; English.

CC The invention relates to an isolated, purified or recombinant  
CC antithrombotic enzyme which hydrolyses fibrin, dissolves blood clots and  
CC prevents platelet aggregation. The enzyme is useful for treating or  
CC preventing a thrombotic related disease in a mammal, such as myocardial  
CC infarction, restenosis, unstable angina or cerebral thrombosis. This  
CC sequence represents a snake antithrombotic enzyme B chain. (updated on 21-  
CC OCT-2003 to standardise OS field)

**SQ** Sequence 146 AA;

```

Query Match          30.3%; Score 210.5; DB 7; Length 146;
Best Local Similarity 37.6%; Pred. No. 4.2e-16;
Matches 47; Conservative 23; Mismatches 46; Indels 9; Gaps 5;

QY      3 ECPGWSSTDRVCYPKFKQEMTWASAEKFCPSQAKGHL-LSVETALBASFDVNLYANKE 61
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db      DCPSEMSVEGHCKYKPFDEPTWDAEKFCTQHKGSHLPLTAVARAIYXXXXGHVDHTKL 83
QY      62 EYLTV---RYTWIGLRVONKKQPCSSISEYNLDVFEECFMWISRDTRLREMEFKVDCEQHS 117
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db      KLIILIGLKNIWNG--CYMKWSDTKLPDKWMREQFEC-LVSR-TVNNEMLSMDCGTTCS 139
OY      118 FICKP 122
       |:|::|
Db      140 FVCKP 144

RESULT 49
AAR24427 standard; protein; 116 AA.
AAR24427
AC      AAR24427;
XX
PT      25-MAR-2003 (revised)
DT      21-NOV-1992 (first entry)
DE      Sequence of the platelet glycoprotein GPIIb inhibitor beta chain (CHH-B-beta).
XX
KM      Platelet adherence inhibitor; platelet anti-adhesive;
KM      antithrombotic agent; von Willebrand Factor;
KM      platelet glycoprotein GPIIb-IX complex.
XX
OS      Crocatus horridus horridus.
XX
PN      MO9208472-A1.
XX
PD      29-MAY-1992.
XX
PP      14-NOV-1991; 91WO-US008516.
XX
PR      16-NOV-1990; 90US-00614443.
PA      (CORT-) COR THERAPEUTICS INC.
PI      Scarborough RM;
PI
DR      WI; 1992-199936/24.
PS
PT      The PAA was purified from a solution of snake venom. Analysis of the peak
CC      inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with
CC      a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin
CC      induced platelet agglutination. They were called CHH-A and CHH-B. The
CC      earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-alpha)
CC      were individually submitted to N-terminal sequence analysis. The
CC      complete amino acid sequence for the alpha and beta chains are given in
CC      AAR24426 and AAR24427. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 116 AA;
QY      Query Match          30.1%; Score 209; DB 2; Length 116;
       Best Local Similarity 37.1%; Pred. No. 4.2e-16;
       Matches 46; Conservative 26; Mismatches 40; Indels 12; Gaps 6;

3 ECPGWSSTDRVCYPKFKQEMTWASAEKFCPSQAKGHLISVETALBASFDVNLYANKE 62
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
DCPSEMSVEGHCKYKPFDEPTWDAEKFCTQHKGSHLPLTAVARAIYXXXXGHVDHTKL 57

```

[illegible]

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QY 114 OQHSTFCCK 121  
DB 121 QONPFVCE 128

## RESULT 2

botroccetin alpha chain - jararaca  
N/Alternate names: two chain botroccetin alpha chain  
C/Species: Bothrops jararaca (jararaca)  
C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A47267, B37958

R/Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A/Title: Primary structure of two-chain botroccetin, a von Willebrand factor modulator protein  
A/Reference number: A47267, PMID:93157385, PMID:8430107

A/Accession: A47267

A/Molecule type: protein

A/Residues: 1-133 <USA>

A/Cross-references: UNIPROT:P22029

A/Experimental source: venom  
A/Note: sequence extracted from NCBI backbone (NCBI:P124085)

R/Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug  
Biochemistry 30, 1957-1964, 1991

A/Title: Isolation and chemical characterization of two structurally and functionally di  
A/Reference number: A37958, PMID:91129280, PMID:1993206

A/Accession: B37958

A/Molecule type: protein

A/Residues: 1-40 <FRU>

C/Complex: heterodimer of alpha and beta (see PIR:B47267) chains

C/Suprafamily: tetraneurin, C-type lectin homology

C/Keywords: hemagglutinin, heterodimer, venom

F/2-128/Domains: C-type lectin homology <LCH>

F/2-13,30-128,103-120/Disulfide bonds: #status experimental

F/80/Disulfide bonds: interchain (to beta-75) #status experimental

Query Match 44.7%; Score 311; DB 2; Length 133;  
Best Local Similarity 45.9%; Pred. No. 3e-25;  
Matches 61; Conservative 24; Mismatches 38; Indels 10; Gaps 3;

QY 62 EVLTRYIYIGLRVYQNGQPC-----SSISYENLVDPF--ECFVWSRDTRLREMFKVDG 112

DB 61 QSSDIYAWIGLRVYQNGQPC-----SSISYENLVDPF--ECFVWSRDTRLREMFKVDG 120

QY 113 EQHSTFCCK 125

DB 121 AQKNPFVCKSP 133

RESULT 3

coagulation factor IX/factor X-binding protein chain A precursor - habu

C/Species: Trimeresurus flavoviridis (habu)  
C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: J04690, A39332

R/Matsuoka, R.; Yoshitake, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.  
Biochem. Biophys. Res. Commun. 220, 382-387, 1996

A/Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from B  
A/Reference number: J04690, PMID:86184662, PMID:8645314

A/Accession: J04690

A/Molecule type: mRNA

A/Residues: 1-152 <MAT>

A/Cross-references: UNIPROT:P23806, DDBJ:D83331, NID:G1402639, PDB:1BA1187.1, PID:G140

A/Experimental source: venom  
R/Atoda, H.; Hyuga, M.; Morita, T.  
J. Biol. Chem. 266, 14903-14911, 1991

A/Title: The primary structure of coagulation factor IX/factor X-binding protein isolate  
protein, tetraneurin, and lymphocyte R<sub>c</sub> coagulation receptor for immunoglobulin E.  
A/Reference number: A39332, PMID:91332000, PMID:1831197

A/Accession: A39332  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 24-152 <ATO>

C/Suprafamily: tetraneurin, C-type lectin homology

C/Keywords: anticoagulant, blood coagulation, glycoprotein, hemolymph, lectin

F/1-23/Domains: signal sequence #status predicted <SIG>

F/24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>

F/25-150/Domains: C-type lectin homology <LCH>

F/25-36,53-150,125-142/Disulfide bonds: #status predicted

Query Match 43.5%; Score 302.5; DB 2; Length 152;  
Best Local Similarity 44.5%; Pred. No. 2.7e-24;  
Matches 57; Conservative 25; Mismatches 37; Indels 9; Gaps 2;

QY 3 ECPGMSSTDRYCYKPFQEMTWASAEFCSEQAKGHLSTVETALASFPDNLVYANK 62

DB 24 DCLSGMSSTYEGHCYAFKFKTWEDAEVCTEQAGAHVLSSESGEADFAVQLVYQNK 83

QY 63 YLTRYIYIGLRVYQNGQPC-----SSISYENLVDPF--CFVWSRDTRLREMFKVDCE 113

DB 84 RLDFYIYIGLRVYQNGQPC-----SSISYENLVDPF--CFVWSRDTRLREMFKVDCE 143

QY 114 OQHSTFCCK 121

DB 144 QONPFVCE 151

RESULT 4

agglutinin alpha chain precursor - sharp-nosed viper

N/Alternate names: fibrinogenolytic venom protein

C/Species: Agkistrodon acutus (sharp-nosed viper)  
C/Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: J07134, PC7037

R/Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.  
Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A/Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom  
A/Reference number: J07134, PMID:20025379, PMID:10558903

A/Accession: J07134

A/Molecule type: mRNA

A/Residues: 1-152 <CHE>

A/Cross-references: UNIPROT:Q9DEF9, UNIPROT:Q9IAM1, UNIPROT:Q6J1W0, GB:AF176420

A/Experimental source: venom gland

A/Accession: PC7037

A/Molecule type: protein

A/Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>

C/Suprafamily: tetraneurin, C-type lectin homology

C/Keywords: disulfide bond, heterodimer, venom

F/1-23/Domains: signal sequence #status predicted <SIG>

F/24-152/Product: agglutinin alpha chain #status experimental <MAT>

Query Match 41.9%; Score 291.5; DB 2; Length 152;  
Best Local Similarity 43.8%; Pred. No. 3.8e-23;  
Matches 56; Conservative 23; Mismatches 40; Indels 9; Gaps 2;

QY 3 ECPGMSSTDRYCYKPFQEMTWASAEFCSEQAKGHLSTVETALASFPDNLVYANK 62

DB 24 DCLSGMSSTYEGHCYAFKFKTWEDAEVCTEQAGAHVLSSESGEADFAVQLVYQNK 83

QY 63 YLTRYIYIGLRVYQNGQPC-----SSISYENLV--DPFVWSRDTRLREMFKVDCE 113

DB 84 SAKIHVWIGLRVYQNGQPC-----SSISYENLV--DPFVWSRDTRLREMFKVDCE 143

QY 114 OQHSTFCCK 121

DB 144 QONPFVCE 151

RESULT 5

agglutinin alpha chain - Malayan pit viper (fragment)

C/Species: Calloselasma rhodostoma (Malayan pit viper)

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: PC7027

R/Chung, C.H.; Au, L.C.; Huang, T.F.

Biochem. Biophys. Res. Commun. 263, 723-727, 1999

C/Title: Molecular cloning and sequence analysis of aggrecan, a collagen-like platelet

A/Reference number: PC7027; PMID:99443731; PMID:10512747

A/Accession: PC7027

A/Molecule type: mRNA

A/Residues: 1-144 <CHU>

A/Cross-references: UNIPROT:Q91841

A/Experimental source: venom gland

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: disulfide bond; platelet aggregation; venom

Query Match 41.4%; Score 288; DB 2; Length 144;

Best Local Similarity 43.8%; Pred. No. 8.3e-23; Indels 12; Gaps 4;

Matches 57; Conservative 21; Mismatches 40; Indels 12; Gaps 4;

QY 3 ECPGWSSTDRYCYKPKQEMTWASAEPCSEQAKGSHLSVETALASFDVNLVYANKE 62

DB 12 DCGFGSPYDQHCYQAFNEQKTWDEAKKFCRAQENGAHLASISNGEADPV-SMLISQKD 70

QY 63 YLT-RIYTWIGLARVONKQGPC-----SSISTENLVDP-PECFMVSRTDRLREMPKY 111

DB 71 ELADEDYVWIGLARVONKQGPCSSSEWSDSSVSYENLIDHTKKCGALEKLTGFRKWNVY 130

QY 112 CEQSHFICK 121

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

DB 131 CEQSHFICK 140

QY 131 CEQSHFICK 140

JC5058: bitiscetin alpha chain - puff adder

N/Alternate names: von Willebrand factor modulator protein

C/Species: Bitis arietans (puff adder)

C/Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004

C/Accession: JC5058; JC5916

R/Matsui, T.; Hamako, J.; Suzuki, M.; Hayaashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz

submitted to JIPID, January 1997

A/Description: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor

A/Reference number: JC5058

A/Contents: snake venom

A/Accession: JC5058

A/Molecule type: protein

A/Residues: 1-131 <MAT>

A/Cross-references: UNIPROT:Q7LZK5

A/Experimental source: snake venom

R/Matsui, T.; Hamako, J.; Suzuki, M.; Hayaashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz

Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997

A/Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modu

A/Reference number: JC5916

A/Accession: JC5916

A/Molecule type: protein

A/Residues: 1-131 <MA2>

A/Experimental source: venom

C/Comment: This protein is a modulator of a von Willebrand factor modulator.

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: venom

F/4-125/Domain: C-type lectin homology <LCH>

Query Match 34.9%; Score 242.5; DB 2; Length 131;

Best Local Similarity 38.5%; Pred. No. 4.3e-18;

Matches 52; Conservative 23; Mismatches 45; Indels 15; Gaps 4;

QY 1 DLCPGWSSTDRYCYKPKQEMTWASAEPCSEQAKGSHLSVETALASFDVNLVYAN 60

DB 1 DPCELDWSSYKCHCYKFKVGTWDEAKKFCVENS--GHLSIDSKKEADFTKLA--- 55

QY 61 KEYLTRYI---WTGLRVONKQGPC-----SSISTENLVDP-PECFMVSRTDRLREMPKY 110

DB 56 SQRLTFRVDAWIGLDESKTQCPQMTDGSVSYENVDPEFKCGLDVHTRYRTIDL 115

QY 111 DCEQSHFICKFTRP 125

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

DB 116 PCEGKNPFICKRSLP 130

QY 116 PCEGKNPFICKRSLP 130

Db 82 LKANLWVWGL--SNVHGNCWQMSDARLNYKDWQWQSSC-LAFRGVH-TEWIMNDCCST 137

Qy 116 HSFICKF 122

Db 138 CSFVCKF 144

# RESULT 9

coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper

C/Species: Viper russelli (Russell's viper)

C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: B42972

R/Name: H.; Mishida, S.; Miyata, T.; Kawada, S.; Salsaka, Y.; Morita, T.; Iwanaga, S.

J. Biol. Chem. 267, 14109-14117, 1992

A/Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no

A/Reference number: A42972; MUID:92332516; PMID:1629211

A/Contents: V. r. slamenis

A/Accession: B42972

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-123 <TRK>

A/Cross-references: UNIPROT:Q7L272

A/Experimental source: venom

A/Note: sequence extracted from NCBI backbone (NCBI:108408)

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: hydrolase; metalloproteinase; venom; zinc

F/4-12/Domain: C-type lectin homology <LCH>

F/4-15,32-121,98-113/Disulfide bonds: #status predicted

Query Match 31.4%; Score 218.5; DB 2; Length 123;

Best Local Similarity 35.9%; Pred. No. 1,3e-15;

Matches 46; Conservative 21; Mismatches 48; Indels 13; Gaps 4;

Qy 2 LKPSGMSSTDRCYCYPFKQEMTWASAEFCSQAGHLLSVETLLEASFDVNVLYANK 61

Db 2 LKPSGMSSTDRCYCYPFKQEMTWASAEFCSQAGHLLSVETLLEASFDVNVLYANK 61

Qy 62 EYLRVYIWGLRVQNGQPC-----SSISYENVLPDFCFWVSDBTRLREWFKYDCEQ 114

Db 62 EYLRVYIWGLRVQNGQPC-----SSISYENVLPDFCFWVSDBTRLREWFKYDCEQ 114

Qy 115 QHSFICKF 122

Db 116 IAPVCKF 123

# RESULT 10

JC5059

bitiscetin beta chain - puff adder

C/Species: Bitis arietans (puff adder)

C/Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004

C/Accession: JC5059; JC5917

R/Name: T.; Hamako, U.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz

submitted to JIPID, January 1997

A/Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor

A/Reference number: JC5058

A/Accession: JC5059

A/Molecule type: protein

A/Residues: 1-125 <MAT>

A/Cross-references: UNIPROT:Q7L2K8

A/Experimental source: snake venom

R/Name: T.; Hamako, U.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz

Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997

A/Title: Complete amino acid sequence of bitiscetin, a novel von willebrand factor modul

A/Reference number: JC5916

A/Accession: JC5917

A/Molecule type: protein

A/Residues: 1-125 <MA2>

A/Experimental source: venom

C/Comment: This protein is a modulator of a von Willebrand factor modulator.

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: venom

F/4-121/Domain: C-type lectin homology <LCH>

Query Match 28.3%; Score 196.5; DB 2; Length 125;

Best Local Similarity 34.1%; Pred. No. 2,6e-13;

Matches 44; Conservative 22; Mismatches 50; Indels 13; Gaps 4;

Qy 1 DLEPSSGMSSTDRCYCYPFKQEMTWASAEFCSQAGHLLSVETLLEASFDVNVLYANK 60

Db 1 DEGLPDMSSYKGHCKYKFKETWADAEKCEKELVNGGHILSVNSREGEFISKL--AL 58

Qy 61 KEYLRYIWIWGLRVQNGQPC-----SSISYENVLPDFCFWVSDBTRLREWFKYDCEQ 113

Db 59 EKMRIYIWIWGL--SHWRICPLRWTDGARDLSDPEICFA--ESFHNKIQTWN 114

Qy 114 QHSFICKF 122

Db 115 RKKSIVCKY 123

# RESULT 11

JC4691

coagulation factor IX/factor X-binding protein chain A precursor - habu

C/Species: Trimeresurus flavoviridis (habu)

C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C/Accession: JC4691; B39332; JC4330

R/Name: R.; Yoshitake, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996

A/Title: cDNA cloning of IX-X-BP, a heterogeneous two-chain anticoagulant protein from br

A/Reference number: JC4690; MUID:96184662; PMID:8645314

A/Accession: JC4691

A/Molecule type: mRNA

A/Residues: 1-146 <MAT1>

A/Cross-references: UNIPROT:P23807; DDBJ:D83332; NID:G1402641; PIDN:BA11868.1; PID:G1402

A/Experimental source: venom

R/Name: R.; Hyuga, M.; Morita, T.

J. Biol. Chem. 266, 14903-14911, 1991

A/Title: The primary structure of coagulation factor IX/factor X-binding protein isolated

from a snake venom, and lymphocyte PC epsilon receptor for immunoglobulin E.

A/Reference number: A39332; MUID:91332000; PMID:1831197

A/Accession: B39332

A/Molecule type: protein

A/Residues: 24-146 <ATD>

R/Name: R.; Ishikawa, M.; Yoshitake, E.; Sekiya, F.; Morita, T.

J. Biochem. 118, 965-973, 1995

A/Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav

A/Reference number: JC4329; MUID:96318509; PMID:8749314

A/Accession: JC4330

A/Molecule type: protein

A/Residues: 24-146 <ATD>

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: anticoagulant; blood coagulation; lectin; venom

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-146/Domain: factor IX/X binding protein chain B #status predicted <MAT>

F/25-142/Domain: C-type lectin homology <LCH>

F/25-36,53-142,119-134/Disulfide bonds: #status predicted

Query Match 27.7%; Score 192.5; DB 2; Length 146;

Best Local Similarity 33.1%; Pred. No. 8,1e-13;

Matches 42; Conservative 22; Mismatches 50; Indels 13; Gaps 4;

Qy 3 ECPSSGMSSTDRCYCYPFKQEMTWASAEFCSQAGHLLSVETLLEASFDVNVLYANK 62

Db 24 DCPSSMSYEGHCYKFPSPKRWADAENCTQOHGHLVFSQSSSEADV--VLAFT 81

Qy 63 YLTRYIWIWGLRVQNGQPC-----SSISYENVLPDFCFWVSDBTRLREWFKYDCEQ 115

Db 82 FGHSLFWWGL--SNVWQNCWQMSDARLNYKDWQWQSSC-LAFRGVH-TEWIMNDCCST 137

Qy 116 HSFICKF 122

Db 138 AQVCECF 144

RESULT 12  
B47267  
botrocetin beta chain - jararaca  
N:Alternate names: two chain botrocetin beta chain  
C/Species: Bothrops jararaca (Jararaca)  
C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B47267, C37958  
R:Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993  
A>Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu  
A/Reference number: A47267, PMID:93157385; PMID:8430107  
A/Accession: B47267  
A:Molecule type: protein  
A:Residues: 1-125 <USA>  
A:Cross-references: UNIPROT:P22030  
A:Experimental source: venom  
A/Note: Sequence extracted from NCBI backbone (NCBI:P124086)  
R:Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug  
Biochemistry 30, 1957-1964, 1991  
A>Title: Isolation and chemical characterization of two structurally and functionally di  
A/Reference number: A37958, PMID:91129280; PMID:1393206  
A/Accession: C37958  
A:Molecule type: protein  
A:Residues: 1-40 <FUJ>  
C/Complex: heterodimer of alpha (see PIR:A47267) and beta chains  
C:Superfamily: tetranectin; C-type lectin homology  
C/Keywords: hemagglutinin; heterodimer; venom  
R:2-121/Domain: C-type lectin homology <LCH>  
R:2-13,30-12,98-113/Disulfide bonds: #status experimental  
F:75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 27.6%; Score 191.5; DB 2; Length 125;  
Best Local Similarity 35.1%; Pred. No. 8.6e-13;  
Matches 46; Conservative 25; Mismatches 41; Indels 19; Gaps 8;  
QY 3 ECPGWSSTDRYCYKPKQEMTWASAEFCSEQAKGHLISVETALASFDVNLVANKK 62  
Db 1 DCPBMSVYEGHCYKRFKEMWMDABEFCTEQTGHLVSPQSKEDADVRSL---TSE 57  
QY 63 YLT-RITWIGLR-VONKQPC-----SSISYEN-LVDPFCFMSRDTLRLEWPKVD 111  
Db 58 MKMGDVVMWIGLSDVMNK---CRFEWTDGMEDYDDYLLAEVYC-VASKEFTN-NKMWIIP 112  
QY 112 CEQGSFICKF 122  
Db 113 CTREKNFVCEP 123  
RESULT 13  
JC2415  
echicetin beta chain - saw-scaled viper  
C/Species: Echis carinatus (saw-scaled viper)  
C/Date: 21-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C/Accession: JC2415  
R:Peng, M.; Holt, J.C.; Mlewiatowski, S.  
Biochem. Biophys. Res. Commun. 205, 68-72, 1994  
A>Title: Isolation, characterization and amino acid sequence of echicetin beta subunit,  
A/Reference number: JC2415; PMID:95091801; PMID:7999097  
A/Accession: JC2415  
A:Molecule type: protein  
A:Residues: 1-123 <PEN>  
A:Cross-references: UNIPROT:P81996  
A:Experimental source: venom  
C/Comment: This protein inhibits agglutination of fixed platelets induced by several pla  
l1ebrand factor and albosagregins.  
C:Superfamily: tetranectin; C-type lectin homology  
C/Keywords: anticoagulant; dimer  
R:2-119/Domain: C-type lectin homology <LCH>  
R:2-11,30-119,96-111/Disulfide bonds: #status predicted  
Query Match 25.8%; Score 179.5; DB 2; Length 123;  
Best Local Similarity 30.4%; Pred. No. 1.5e-11;

Matches 38; Conservative 23; Mismatches 51; Indels 13; Gaps 4;  
QY 4 CPGWSSTDRYCYKPKQEMTWASAEFCSEQAKGHLISVETALASFDVNLVANKK 63  
Db 2 CLPBMVYEGHCYKRFKEMWMDABEFCTEQTGHLVSPQSKEDADVRSL---TSE 57  
QY 64 LRRYIWIWIGLR-VONKQPC-----SSISYEN-LVDPFCFMSRDTLRLEWPKVD 116  
Db 61 -MELVWIGL--SDYRDCYWNESDGLDYKAWDNRHCF--AAKTTDNQWMRKSGER 115  
QY 117 SFICK 121  
Db 116 YFVCK 120

RESULT 14  
S56006  
tokaracetin alpha chain - Trimeresurus tokarensis (fragment)  
N:Alternate names: platelet aggregation inhibitor; platelet antagonist  
C/Species: Trimeresurus tokarensis  
C/Date: 10-Oct-1995 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: S56006  
R:Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai,  
Biochem. J. 308, 947-953, 1995  
A>Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib ar  
A/Reference number: S56006, PMID:97104297; PMID:8948455  
A/Accession: S56006  
A:Molecule type: protein  
A:Residues: 1-40 <KAW>  
A:Cross-references: UNIPROT:Q7L2K6  
C:Superfamily: tetranectin; C-type lectin homology

Query Match 24.2%; Score 168; DB 2; Length 40;  
Best Local Similarity 70.0%; Pred. No. 6.9e-11;  
Matches 28; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 3 ECPGWSSTDRYCYKPKQEMTWASAEFCSEQAKGHL 42  
Db 1 DCPBMSVYEGHCYKRFKEMWMDABEFCTEQTGHLV 40

RESULT 15  
RGH1A  
regenerating islet lectin 1-alpha precursor [validated] - human  
N:Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg1-a)  
N/Contains: pancreatic stone protein (PSP)  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1990 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C/Accession: A35197, B28351, S12950, S02767, S02419, S00113, S01471, A25246  
R:Matanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.  
J. Biol. Chem. 265, 7432-7439, 1990  
A>Title: Complete nucleotide sequence of human reg gene and its expression in normal and  
product of the gene.  
A/Reference number: A35197; PMID:90237042; PMID:2332435  
A/Accession: A35197  
A:Molecule type: DNA  
A:Residues: 1-166 <WAT>  
A:Cross-references: UNIPROT:P05451; GB:J05412  
R:Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto,  
J. Biol. Chem. 263, 2111-2114, 1988  
A>Title: A novel gene activated in regenerating islets.  
A/Reference number: A92704; PMID:88115343; PMID:2563000  
A/Accession: B28351  
A:Molecule type: mRNA  
A:Residues: 1-166 <TER>  
A:Cross-references: UNIPROT:P05451; PID:AAA6558.1; PID:G190979  
R:Ittoh, T.; Tanuki, H.; Katoh, T.; Teraoka, H.; Matsumoto, K.; Yoshida, N.; Terazono, K.  
FEBS Lett. 272, 85-88, 1990  
A>Title: Isolation and characterization of human reg protein produced in Saccharomyces ce  
A/Reference number: S12950; PMID:91032149; PMID:2226837  
A/Accession: S12950  
A:Molecule type: protein  
A:Residues: 23-52;160-166 <ITO>

A>Note: sequence determined from protein isolated after human CDNA sequence was cloned a  
 Ride Caro, A.M.; Adich, Z.; Fournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Rovey  
 Blochm. Biophys. Acta 994, 281-284, 1999  
 A>Title: N-terminal sequence extension in the glycosylated forms of human pancreatic stc  
 A:Reference number: S024197, PMID:89150292, PMID:2493268  
 A:Accession: S024197  
 A:Molecule type: protein  
 A:Residues: 23-47 <DEC>  
 R:Roumi, P.; de Caro, J.; Bonicel, J.; Rovey, M.; de Caro, A.  
 FEBS Lett. 229, 171-174, 1988  
 A>Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone pro  
 A:Reference number: S024197, PMID:88029417, PMID:3345835  
 A:Accession: S024197  
 A:Molecule type: protein  
 A:Residues: 63-72;125-139;150-157;160-166 <ROU>  
 A>Note: disulfide bonds  
 A:de Caro, A.M.; Bonicel, J.J.; Roumi, P.; de Caro, J.D.; Sarles, H.; Rovey, M.  
 Eur. J. Biochem. 168, 201-207, 1987  
 A>Title: Complete amino acid sequence of an immunoreactive form of human pancreatic ston  
 A:Reference number: S00113, PMID:88029417, PMID:3655916  
 A:Accession: S00113  
 A:Molecule type: protein  
 A:Residues: 34-166 <DEB>  
 R:Roumi, P.; Bonicel, J.; Rovey, M.; de Caro, A.  
 FEBS Lett. 216, 195-199, 1987  
 A>Title: Cleavage of the Arg-116 bond in the native polypeptide chain of human pancreati  
 A:Reference number: S01471, PMID:87219142, PMID:3108036  
 A:Accession: S01471  
 A:Molecule type: protein  
 A:Residues: 33-48 <RO2>  
 R:Montalvo, G.; Bonicel, J.; Multigner, L.; Rovey, M.; Sarles, H.; De Caro, A.  
 Biochem. J. 238, 227-232, 1986  
 A>Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancreat  
 A:Reference number: A25246, PMID:8709950, PMID:3541906  
 A:Accession: A25246  
 A:Molecule type: protein  
 A:Residues: 34-73;75-87;89-98 <MON>  
 C:Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like clea  
 C:Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the growth  
 C:Genetics:  
 A:Gene: GDB:REG1A; REG  
 A:Cross-references: GDB:132455; OMIM:167770  
 A:Map position: 2p12-2p12  
 A:Mutons: 22/1; 61/3; 107/3; 145/1  
 C:Superfamily: tetralectin; C-type lectin homology  
 C:Keywords: glycoprotein; lectin; pancreas; pyroglytamic acid  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:1-23-166/Product: regenerating islet lectin 1-alpha #status experimental <MAT>  
 F:134-166/Product: pancreatic stone protein #status experimental <MAT>  
 F:136-162/Domain: C-type lectin homology <LCH>  
 F:23/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimen  
 F:27/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:33-44/Cleavage site: Arg-116 (tryptic) #status experimental  
 F:36-47,64-162,137-154/Disulfide bonds: #status experimental

Query Match 24.2%; Score 168; DB 1; Length 166;  
 Best Local Similarity 31.1%; Pred. No. 3.4e-10;  
 Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

QY 2 LKPSGMSSTDRYCYKPFQEMTWASAEFSCGQAKGHLSEVETALASFPDNLVYANK 61  
 DB 34 ISCPGETNAYRSYCYFNEDETRTWADDDYC-QNNNSGNTVSVLTQAEQAFVASTL--K 89  
 QY 62 EYLTR--YIWIIGLRVONKQ-----PCSSISYE-----NLVDPFECFMSRDTLRLRM 107  
 DB 90 ESGTDDFNWVIGLHDPKKNRMRHWSGSLVYSKMGIGAPSSVNPQVSLTSSIGFQKM 149  
 QY 108 FKYVDEQGHSTFCKF 122  
 DB 150 KDVPCEDKFSPVCKF 164

RESULT 16

A45751  
 Pancreatic stone protein precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jul-2004  
 C:Accession: A45751  
 R:Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J.; Sarles, H.; Dagorn, J.C.  
 J. Clin. Invest. 84, 100-106, 1989  
 A>Title: Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and expres  
 A:Reference number: A45751, PMID:89292148, PMID:2525567  
 A:Accession: A45751  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-166 <GIO>  
 A:Cross-references: UNIPROT:P05451; GB:M27190, NID:9623412; PIDN:AAA60546.1; PID:9623413  
 C:Superfamily: tetralectin; C-type lectin homology  
 F:36-162/Domain: C-type lectin homology <LCH>

Query Match 24.2%; Score 168; DB 2; Length 166;  
 Best Local Similarity 31.1%; Pred. No. 3.4e-10;  
 Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

QY 2 LKPSGMSSTDRYCYKPFQEMTWASAEFSCGQAKGHLSEVETALASFPDNLVYANK 61  
 DB 34 ISCPGETNAYRSYCYFNEDETRTWADDDYC-QNNNSGNTVSVLTQAEQAFVASTL--K 89  
 QY 62 EYLTR--YIWIIGLRVONKQ-----PCSSISYE-----NLVDPFECFMSRDTLRLRM 107  
 DB 90 ESGTDDFNWVIGLHDPKKNRMRHWSGSLVYSKMGIGAPSSVNPQVSLTSSIGFQKM 149  
 QY 108 FKYVDEQGHSTFCKF 122  
 DB 150 KDVPCEDKFSPVCKF 164

RESULT 17

S29822  
 pancreaticis-associated protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S29822  
 R:Itob, T.; Terakura, H.  
 Biochim. Biophys. Acta 1172, 184-186, 1993  
 A>Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homology  
 A:Reference number: S29821; PMID:93176807, PMID:7679928  
 A:Accession: S29822  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-175 <IRO>  
 A:Cross-references: UNIPROT:P35230; GB:D13509, NID:9286106; PIDN:BA02727.1; PID:9286107  
 C:Superfamily: tetralectin; C-type lectin homology  
 F:40-171/Domain: C-type lectin homology <LCH>

Query Match 23.7%; Score 164.5; DB 2; Length 175;  
 Best Local Similarity 30.0%; Pred. No. 8.3e-10;  
 Matches 42; Conservative 20; Mismatches 57; Indels 21; Gaps 4;

QY 2 LKPSGMSSTDRYCYKPFQEMTWASAEFSCGQAKGHLSEVETALASFPDNLVYANK 60  
 DB 38 ISCPGSGQAYGSCYALPQITWPDALAC-QKRPQGLVSLVMSAEASFLSSVVKRTG 96  
 QY 61 KYILRYIWIIGLRVONKQPCSSISYE-----NLVDPFECFMSRDTLRLRM 103  
 DB 97 NSY--QYIWIIGLHDPKKNRMRHWSGSLVYSKMGIGAPSSVNPQVSLTSSIGFQKM 154  
 QY 104 LKPFVDEQGHSTFCKF 123  
 DB 155 FLKMRDMTCVGLPYVCKF 174

RESULT 18

B47148  
 reg II, regenerating islet cells - mouse  
 C:Species: Mus musculus (house mouse)











AS4423  
Brevican precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: AS4423; S41914  
R:Yamada, H.; Matanabe, K.; Shimomura, M.; Yamaguchi, Y.  
J: Biol. Chem. 269, 10119-10126, 1994  
A:Title: Molecular cloning of brevican, a novel brain proteoglycan of the aggrecan/versican family  
A:Reference number: AS4423; MUID:94193597; PMID:8145412  
A:Accession: AS4423  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-912 <YAM>  
A:Cross-references: UNIPROT:Q28062; GB:X75887; NID:9452820; PIDN:CA53481.1; PID:9452821  
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG  
F:50-139/Domain: immunoglobulin homology <IM>  
F:174-251/Domain: link protein repeat homology <LNK1>  
F:272-353/Domain: link protein repeat homology <LNK2>  
F:651-682/Domain: EGF homology <EGF>  
F:689-809/Domain: C-type lectin homology <LCH>  
F:816-872/Domain: complement factor H repeat homology <FHD>

Query Match 20.6%; Score 143.5; DB 2; Length 912;  
Best Local Similarity 28.8%; Pred. No. 8,2e-07;  
Matches 46; Conservative 10; Mismatches 51; Indels 53; Gaps 7;

QY 4 CPSSGMSSTRDYCYKPFQKMTWASAEFCSEAQKAGHLSVETALASFDVNVLYANKE 63  
DB 689 GSPGMDAFQGCYKHSARSSEAEENKC--RMYGHLASISPEEDPTNN-----R 739  
QY 64 LRRYIWIIGLRVQ-----NKGPCSS-SISEYLVDFECCMYSRDR 103  
DB 740 YREYQWIGLNDRTIEGDFRMSDGPVLLYNNMFGQDPSYFLGECNV-----VMWHDQ- 793  
QY 104 LREMFVDEQGHSPICK-----FTRPR 126  
DB 794 -GQMSDVPNCVNYHLSYCKNGLVSCGPPPLALAEVGRFR 832

RESULT 27  
A28452  
proteoglycan core protein precursor, cartilage - rat  
N:Alternate names: aggrecan  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A92623; A23835; A28095; A28452  
R:Doerge, K.; Saasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.  
J: Biol. Chem. 262, 17757-17767, 1987  
A:Title: Complete primary structure of the rat cartilage proteoglycan core protein deduced from complementary DNA  
A:Reference number: A92623; MUID:88087070; PMID:3693370  
A:Accession: A92623  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2124 <DOE>  
A:Cross-references: UNIPROT:P07897  
R:Doerge, K.; Saasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.  
J: Biol. Chem. 263, 100404, 1988  
A:Reference number: A9069  
A:Contents: annotation; revision to residue 698  
R:Doerge, K.; Fernandez, P.; Hassell, J.R.; Saasaki, M.; Yamada, Y.  
J: Biol. Chem. 261, 8108-8111, 1986  
A:Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat core protein  
A:Reference number: A23835; MUID:86250698; PMID:2424893  
A:Accession: A23835  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1856-2124 <DOE>  
A:Cross-references: GB:M1518; NID:9206104; PIDN:AAA1836.1; PID:9206105  
R:Neame, P.J.; Christner, J.E.; Baker, J.R.  
J: Biol. Chem. 262, 17768-17778, 1987  
A:Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term  
A:Reference number: A28453; MUID:88087071; PMID:3693371  
A:Accession: A28453  
A:Molecule type: protein  
A:Residues: 20-37, W',39-60, 'E',62-64, 'X',66-69;70-83;84,89-148, 'L',150-238, 'S',240, 'A',

C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF  
C:Keywords: glycoprotein  
F:1-13/Domain: signal sequence #status predicted <SIG>  
F:20-212/Domain: proteoglycan core protein #status predicted <MAT>  
F:44-135/Domain: immunoglobulin homology <IM>  
F:170-247/Domain: link protein repeat homology <LNK1>  
F:268-349/Domain: link protein repeat homology <LNK2>  
F:504-581/Domain: link protein repeat homology <LNK3>  
F:602-683/Domain: link protein repeat homology <LNK4>  
F:1914-2034/Domain: C-type lectin homology <LCH>  
F:2041-2097/Domain: complement factor H repeat homology <FHD>  
F:126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.6%; Score 143; DB 2; Length 2124;  
Best Local Similarity 32.3%; Pred. No. 2,4e-06;  
Matches 43; Conservative 12; Mismatches 54; Indels 24; Gaps 7;

QY 3 EPPSSGMSSTRDYCYKPFQKMTWASAEFCSEAQKAGHLSVETALASFDVNVLYANKE 62  
DB 1913 QCEBMTKFGQHCYHFPDRETWDAERCRQO--SHLSIVTEDEQEFV-----NKN 1964  
QY 63 YLRYIWIIGLRVQ-----KQPCSSISYE-----NLVDPF-----ECFVSRDTRLEWF 108  
DB 1965 -AQDYQWIGLNDRTIEGDFRMSDGHSLQPEKRPQPNFATGEDCVVMWHER-GEWN 2022  
QY 109 KVDCEQGHSPICK 121  
DB 2023 DVPNCVNYLPFTCK 2035

RESULT 28  
A55182  
aggrecan precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A55182; S55329; S50207; S51355; I78532; I58123  
R:Malcz, E.; Deak, F.; Ehrhart, P.; Coulter, S.N.; Fuellep, C.; Horvath, P.; Doerge, K.J.;  
Genomics 22, 364-371, 1994  
A:Title: Complete coding sequence, deduced primary structure, chromosomal localization, &  
A:Reference number: A55182; MUID:95104847; PMID:7806222  
A:Accession: A55182  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-2132 <MAL>  
A:Cross-references: UNIPROT:Q61282; GB:L07049; NID:9678541; PIDN:AA37670.1; PID:9191772  
R:Matanabe, H.; Gao, L.; Sugiyama, S.; Doerge, K.; Kimata, K.; Yamada, Y.  
Biochem. J. 308, 433-440, 1995  
A:Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structure  
A:Reference number: S55329; MUID:95289972; PMID:7772024  
A:Accession: S55329  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-567 'G',569-1728 'I',1730-2132 <MAT>  
A:Cross-references: GB:U22901; NID:9886014  
R:Glimoff, V.; Savontaus, M.; Vehanen, J.;  
Biochem. Biophys. Acta 1219, 613-622, 1994  
A:Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by  
A:Reference number: S50206; MUID:95035091; PMID:7524681  
A:Accession: S50207  
A:Molecule type: mRNA  
A:Residues: 350-481, 'R',483-506 <GLU1>  
A:Cross-references: EMBL:X80279; NID:9673432  
R:Glimoff, V.  
submitted to the EMBL Data Library, July 1994  
A:Reference number: S51355  
A:Accession: S51355  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 350-383, 'CPVMSQRRPMAA' <GLU2>  
A:Cross-references: EMBL:X80279  
R:Matanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.  
Nature Genet. 7, 154-157, 1994  
A:Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrec

A:Reference number: 158123; UID:95004579; PMID:7920633  
 A:Accession: 178532  
 A:Species: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-326 <MAT2>  
 A:Cross-references: GB:S73722; NID:g765215; PIDN:AA32160.1; PID:g765216  
 A:Accession: 158123  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-240; 'MCTASLRMRVRSFMRHPOHNSPSRROPT', 'AGMGHAMPPOASSTWPGRAVWTCALAGW', 'R  
 A:Cross-references: GB:S73720; NID:g765211; PIDN:AA32159.1; PID:g765212  
 C:Genetics:  
 A:Map position: 7  
 A:Insertions: 253/1  
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC  
 C:Keywords: cartilage; extracellular matrix  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:144-135/Domain: immunoglobulin homology <IMM>  
 F:170-247/Domain: link protein repeat homology <LNK1>  
 F:268-349/Domain: link protein repeat homology <LNK2>  
 F:504-581/Domain: link protein repeat homology <LNK3>  
 F:602-683/Domain: link protein repeat homology <LNK4>  
 F:1922-2042/Domain: C-type lectin homology <LCH>  
 F:2042-2105/Domain: complement factor H repeat homology <FHD>

Query Match 20.5%; Score 143; DB 1; Length 2132;  
 Best Local Similarity 32.3%; Pred. No. 2.4e-06;  
 Matches 43; Conservative 12; Mismatches 54; Indels 24; Gaps 7;

QY 3 ECPGMSSTDRYCYKPKQEMTASARFCSEQAKGHLISVETALASFDVNLANKY 62  
 DB 1921 QCESEGTKEQGHCHYRFPDETWDAERCREQQ--SHLSIYVPEEQEFV-----NKN 1972  
 QY 63 YLTRYIWIIGLRVQ-----KGPCSSISYE---NLVDPF-----EGFMWSRDTLRERF 108  
 DB 1973 -AODYWGIGLNDFTIGDFRWSGSHLQFEKMRPNPDNPFATGECVWIMHER-GEWN 2030  
 QY 109 KYDCEQHSFICK 121  
 DB 2031 DVPQNYQLPFTCK 2043

RESULT 29  
 S57653  
 A:Reference number: 158123; UID:95004579; PMID:7920633  
 A:Accession: 178532  
 A:Species: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-326 <MAT2>  
 A:Cross-references: GB:S73722; NID:g765215; PIDN:AA32160.1; PID:g765216  
 A:Accession: 158123  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-240; 'MCTASLRMRVRSFMRHPOHNSPSRROPT', 'AGMGHAMPPOASSTWPGRAVWTCALAGW', 'R  
 A:Cross-references: GB:S73720; NID:g765211; PIDN:AA32159.1; PID:g765212  
 C:Genetics:  
 A:Map position: 7  
 A:Insertions: 253/1  
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC  
 C:Keywords: cartilage; extracellular matrix  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:144-135/Domain: immunoglobulin homology <IMM>  
 F:170-247/Domain: link protein repeat homology <LNK1>  
 F:268-349/Domain: link protein repeat homology <LNK2>  
 F:504-581/Domain: link protein repeat homology <LNK3>  
 F:602-683/Domain: link protein repeat homology <LNK4>  
 F:1922-2042/Domain: C-type lectin homology <LCH>  
 F:2042-2105/Domain: complement factor H repeat homology <FHD>

Query Match 20.5%; Score 142.5; DB 2; Length 883;  
 Best Local Similarity 30.6%; Pred. No. 1e-06;  
 Matches 49; Conservative 8; Mismatches 50; Indels 53; Gaps 8;

QY 4 CPBGMSSTDRYCYKPKQEMTASARFCSEQAKGHLISVETALASFDVNLANKY 63  
 DB 664 CSPGMAFPQACVCKHSTRSRSEASQ--RALLGALHTSCTPEEDDFV-----NDRY 715

QY 64 LTRYIWIIGLRVQ-----NKGPCS-SISENLVDPPECRMSRDR 103  
 DB 716 -REYQWIGLNDFTIGDFRWSGSHLQFEKMRPNPDNPFATGECVWIMHER-GEWN 2030  
 QY 104 LREMFVDEQGHFICK-----FTRPR 126  
 DB 769 -GQMSVPCNYHLSTYCKMGLVSCGPPPLQPLAQLFRPR 807

RESULT 30  
 A53210  
 A:Reference number: 158123; UID:95004579; PMID:7920633  
 A:Accession: 178532  
 A:Species: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-326 <MAT2>  
 A:Cross-references: GB:S73722; NID:g765215; PIDN:AA32160.1; PID:g765216  
 A:Accession: 158123  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-240; 'MCTASLRMRVRSFMRHPOHNSPSRROPT', 'AGMGHAMPPOASSTWPGRAVWTCALAGW', 'R  
 A:Cross-references: GB:S73720; NID:g765211; PIDN:AA32159.1; PID:g765212  
 C:Genetics:  
 A:Map position: 7  
 A:Insertions: 253/1  
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC  
 C:Keywords: cartilage; extracellular matrix  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:144-135/Domain: immunoglobulin homology <IMM>  
 F:170-247/Domain: link protein repeat homology <LNK1>  
 F:268-349/Domain: link protein repeat homology <LNK2>  
 F:504-581/Domain: link protein repeat homology <LNK3>  
 F:602-683/Domain: link protein repeat homology <LNK4>  
 F:1922-2042/Domain: C-type lectin homology <LCH>  
 F:2042-2105/Domain: complement factor H repeat homology <FHD>

Query Match 20.5%; Score 142.5; DB 2; Length 1463;  
 Best Local Similarity 26.2%; Pred. No. 1.8e-06;  
 Matches 39; Conservative 25; Mismatches 44; Indels 41; Gaps 8;

QY 4 CPBGMSSTDRYCYKPKQEMTASARFCSEQAKGHLISVETALASFDVNLANKY 58  
 DB 959 CPKGMILPYKCKLLKIPGSPDKMTSADQFCVBE--GGTIVALENEVEQAFITMTLF 1016  
 QY 59 ANKEYLTRYIWIIGLRVQ-----KGPCSSISYE--NLVDPF-----EGFMWSRDTLRERF 108  
 DB 1017 GH-----TTNWWIGLQDDDYDEKMLNGRP--VSYSN--SPFDGNIPIHNTTEYOKRIPLC 1068  
 QY 96 FMWSRDTLRERF-----EGFMWSRDTLRERF 121  
 DB 1069 GLLSNNPNFHTGKWFEDCRGCVFCE 1097

RESULT 31  
 A39086  
 A:Reference number: 158123; UID:95004579; PMID:7920633  
 A:Accession: 178532  
 A:Species: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-326 <MAT2>  
 A:Cross-references: GB:S73722; NID:g765215; PIDN:AA32160.1; PID:g765216  
 A:Accession: 158123  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 211-240; 'MCTASLRMRVRSFMRHPOHNSPSRROPT', 'AGMGHAMPPOASSTWPGRAVWTCALAGW', 'R  
 A:Cross-references: GB:S73720; NID:g765211; PIDN:AA32159.1; PID:g765212  
 C:Genetics:  
 A:Map position: 7  
 A:Insertions: 253/1  
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC  
 C:Keywords: cartilage; extracellular matrix  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:144-135/Domain: immunoglobulin homology <IMM>  
 F:170-247/Domain: link protein repeat homology <LNK1>  
 F:268-349/Domain: link protein repeat homology <LNK2>  
 F:504-581/Domain: link protein repeat homology <LNK3>  
 F:602-683/Domain: link protein repeat homology <LNK4>  
 F:1922-2042/Domain: C-type lectin homology <LCH>  
 F:2042-2105/Domain: complement factor H repeat homology <FHD>

J. Clin. Invest. 89, 1512-1516, 1992  
 A>Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the 1 domain.  
 A/Reference number: A43919; MUID:92235266; PMID:1569188  
 A/Accession: A43919  
 A/Molecule type: protein  
 A/Residues: 361-370, 'X', 372-373, 393-399, 'X', 401-407, 'X', 409 <SN>  
 A/Cross-references: PDB:1AB2079.1; PID:g248844; PDB:1AB2077.1; PID:g248842; PDB:1AB  
 A/Experimental source: synovial fluid  
 A/Note: sequences modified after extraction from NCBI backbone  
 R/Bary, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.  
 Matrix Biol. 14, 323-328, 1994  
 A>Title: Length variation in the keratan sulfate domain of mammalian aggrecan.  
 A/Reference number: 146998; MUID:95128522; PMID:7827755  
 A/Accession: 546659  
 A/Molecule type: DNA  
 A/Residues: 764-765, 'A', 767-846, 'V', 848-862, 'X', 864 <BAR>  
 A/Cross-references: EMBL:S74659; NID:9807127; PDB:1AAC60643.1; PID:9807128  
 A/Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue  
 R/Hic, M.Z.; Mok, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.  
 Arch. Biochem. Biophys. 322, 22-30, 1995  
 A>Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the  
 A/Reference number: 566389; MUID:96004775; PMID:7574678  
 A/Accession: 566389  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 17-23, 24, 'X', 26-27, 393-401, 402-403 <ILI>  
 R/Forsang, A.U.; Lasc, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.  
 FEBS Lett. 380, 17-20, 1996  
 A>Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).  
 A/Reference number: 568646; MUID:96181659; PMID:8603731  
 A/Accession: 568646  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 'V', 404-405, 'XX', <FOS>  
 R/Dudha, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.  
 Biochem. J. 313, 933-940, 1996  
 A>Title: Age-related changes in the content of the C-terminal region of aggrecan in huma  
 A/Reference number: 562786; MUID:96190740; PMID:8611178  
 A/Accession: 562786  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 <DUD>  
 A/Cross-references: EMBL:X17406; NID:930248; PDB:1CAA5463.1; PID:930249  
 R/Baldwin, C.T.; Regnato, A.M.; Prockop, D.J.  
 J. Biol. Chem. 264, 15747-15750, 1989  
 A>Title: A new epidermal growth factor-like domain in the human core protein for the lat  
 A/Reference number: A34226; MUID:89380154; PMID:2789216  
 A/Accession: A34226  
 A/Molecule type: mRNA  
 A/Residues: 1936-1963, 'V', 1965-2069, 'A', 2071-2415 <BAL>  
 A/Cross-references: GB:U05062; NID:9181167; PDB:1AAA35726.1; PID:g181168  
 C/Genetics:  
 A/Gene: GDB:AGC1; CSDP1; CSDPCP; MSK16  
 A/Cross-references: GDB:127479; OMIM:155760  
 A/Map position: 15q26-15q26  
 A/Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG  
 C/Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracell  
 F/1-19/Domain: signal sequence #status predicted <SIG>  
 F/20-2415/Product: aggrecan cartilage long splice form #status predicted <MAT>  
 F/20-2162, 2201-2415/Product: aggrecan cartilage short splice form #status predicted <MAT  
 F/20-2162, 2201-2329, 'A', 2392-2415/Product: aggrecan short splice form #status predicted  
 F/44-115/Domain: immunoglobulin homology <IM>  
 F/170-247/Domain: link protein repeat homology <LNK1>  
 F/268-349/Domain: link protein repeat homology <LNK2>  
 F/495-572/Domain: link protein repeat homology <LNK3>  
 F/593-673/Domain: link protein repeat homology <LNK4>  
 F/677-864/Domain: keratan sulfate attachment #status predicted <KSA>  
 F/864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>  
 F/1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>  
 F/2168-2198/Domain: BGF homology <BGF>  
 F/2205-2325/Domain: C-type lectin homology <LCH>

F/2332-2388/Domain: complement factor H repeat homology <FHD>  
 F/126, 239, 333, 387, 434, 602, 657, 737, 1898/Binding site: carbohydrate (Asn) (covalent) #stat  
 F/312, 376/Binding site: keratan sulfate (Thr) (covalent) #status predicted  
 Query Match 20.4%; Score 142; DB 1; Length 2415;  
 Best Local Similarity 31.3%; Pred. No. 3.5e-06;  
 Matches 42; Conservative 11; Mismatches 53; Indels 28; Gaps 7;  
 QY 4 CPSCGMSSTRDYCYKPFQEMTWASAEERFCSEDAKGGHLLSVETALASFPVDNVLANKY 63  
 DB 2205 CEEGMNKKQGGCHVHPDRFETWDAERCRHQ--SHLSSTVPEEQEFVNN--NAQ- 2257  
 QY 64 LTRYIWTGLRVQ-----NKQPCSTSYENL--VDPECFVNSDPTLR-----EW 107  
 DB 2258 --DYQWIGLMDRTIEGDFRWSGHP--MQFENRPNQPNFPAAGSDCVMTWHEKGEW 2312  
 QY 108 FKVDCEQHSFICK 121  
 DB 2313 NDVPCNHLPTCK 2326  
 RESULT 32  
 T46256  
 Brevican - human (fragment)  
 N/Alternate names: protein DKFZp761L191.1  
 C/Species: Homo sapiens (man)  
 C/Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
 C/Accession: T46256  
 R/Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A/Reference number: 223031  
 A/Accession: T46256  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-330 <AAA>  
 A/Cross-references: UNIPROT:O9NT67; EMBL:AL137504  
 A/Experimental source: adult amygdala; clone DKFZp761L191  
 C/Genetics:  
 A/Note: DKFZp761L191.1  
 C/Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG  
 Query Match 20.4%; Score 141.5; DB 2; Length 330;  
 Best Local Similarity 28.8%; Pred. No. 4.3e-07;  
 Matches 46; Conservative 10; Mismatches 51; Indels 53; Gaps 7;  
 QY 4 CPSCGMSSTRDYCYKPFQEMTWASAEERFCSEDAKGGHLLSVETALASFPVDNVLANKY 63  
 DB 107 CIMPMDAPGACYKAFSTRSRWEAEATQC--RMVGAHLASISTPEEDPFINN-----R 157  
 QY 64 LTRYIWTGLRVQ-----NKQPCSTSYENLVDPECFVNSDPTLR 103  
 DB 158 YREYQWIGLMDRTIEGDFLMSDGVPLVYNNMFGQPDSPFVSGENCV-----VMWHDQ- 211  
 QY 104 LREMFVDCQOHSFICK-----FTFPR 126  
 DB 212 -GQMSDVPNCNHLSTYCKMGVLSGCPPELPLAQVFGRR 250  
 RESULT 33  
 S49126  
 Brevican precursor - rat  
 N/Alternate names: aggrecan-like protein  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
 C/Accession: S49126; I55457  
 R/Seidenbecher, C.I.; Langnaese, K.; Wax, H.; Seidel, B.; Garner, C.C.; Gundelfinger, E.D  
 submitted to the EMBL Data Library, June 1994  
 A/Description: Molecular cloning of a new member of the aggrecan/versican family of prote  
 A/Reference number: S49126  
 A/Accession: S49126  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-883 <SEI>

A:Cross-references: UNIPROT:P55068; EMBL:X79881; NID:G509396; PIDN:CA56255.1; PID:G509396  
 R:Seidenbuecher, I.C.; Richner, K.; Rauch, U.; Fässler, R.; Garner, C.C.; Gundelfinger, E.  
 J. Biol. Chem. 270, 27206-27212, 1995  
 A:Title: Brevican, a Chondroitin Sulfate Proteoglycan of Rat Brain, Occurs as Secreted a  
 A:Reference number: 155457; MUID:96070828; PMID:7592978  
 A:Accession: 155457  
 A:Status: translated from GB/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-883 <RES>  
 A:Cross-references: EMBL:X79881; NID:G509396; PIDN:CA56255.1; PID:G509397  
 C:Comment: For an alternative splice form, see PIR:A53908  
 C:Superfamily: aggrecan, C-type lectin homology; complement factor H repeat homology; EC  
 C:Keywords: alternative splicing  
 F:49-138/Domain: immunoglobulin homology <IMM>  
 F:173-250/Domain: link protein repeat homology <LNK1>  
 F:271-352/Domain: link protein repeat homology <LNK2>  
 F:626-657/Domain: EGF homology <EGF>  
 F:664-784/Domain: C-type lectin homology <LCH>  
 F:791-847/Domain: complement factor H repeat homology <FHD>

Query Match 20.4%; Score 140.5; DB 2; Length 883;  
 Best Local Similarity 30.6%; Pred. No. 1.6e-06;  
 Matches 49; Conservative 7; Mismatches 51; Indels 53; Gaps 8;

QY 4 CP6GMSSTRDYCYKPKQEWMTWASAEFSCSEQAKGHLISVETALASFYDNLVYANKY 63  
 DB 664 CSPGMPFPGACYKHFESTRSWEAESEQ--RALGAHLTSCPEEDQFV-----NDRY 745  
 QY 64 LTRYIYIGLRVQ-----NKGQPS-SISTENLVDPCEFWVSQDTR 103  
 DB 716 -REYQWIGLNDRTIEGDFLWSDGPPILLYENWNPQPSYSLSGNCV-----VWVMDQ- 768  
 QY 104 LREMFVDCSEQHSFICK-----FTRPR 126  
 DB 769 -GGMSDVPCKYHSLYTCMKMLVSGCPPPLPLAQIFGRPR 807

## RESULT 34

A38609  
 lectin, galactose-specific - western diamondback rattlesnake  
 C:Species: Crocatus atrox (western diamondback rattlesnake)  
 C>Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 09-Jul-2004  
 C:Accession: A38609  
 R:Hiirabayashi, J.; Kusunoki, T.; Kasai, K.  
 J. Biol. Chem. 266, 2320-2326, 1991  
 A:Title: Complete primary structure of a galactose-specific lectin from the venom of the  
 A:Reference number: A38609; MUID:9115849; PMID:1989986  
 A:Accession: A38609  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-115 <HIR>  
 A:Cross-references: UNIPROT:P21963  
 C:Superfamily: tetralectin, C-type lectin homology  
 F:3-131/Domain: C-type lectin homology <LCH>  
 F:3-14,31-131,106-123/disulfide bonds: #status predicted

Query Match 20.1%; Score 140; DB 2; Length 135;  
 Best Local Similarity 28.5%; Pred. No. 2.3e-07;  
 Matches 39; Conservative 21; Mismatches 51; Indels 26; Gaps 6;

QY 4 CP6GMSSTRDYCYKPKQEWMTWASAEFSCSEQAKGHLISVETALASFYDNLVYANKY 63  
 DB 3 CPDMLPMNOLCKYRQQLTWDAEMFCYKRGCHLASFHYGSLER-----AEY 55  
 QY 64 LTRYIYIGLRVQ-----GQPCSS-ISYE-NLVDPFE-----CFWVSQDTRL 104  
 DB 56 ISDYHKGQEWVWIGLRKKKDFSEWMTDRSCTDYLTWQKQDPHYQKFCVELVSLGY 115  
 QY 105 REMFVDCSEQHSFICK 121  
 DB 116 RLWMDVCESKDAFLCO 132

## RESULT 35

LNRC1  
 lectin BRA3-1 precursor - barnacle (Megabalanus rosa)  
 C:Species: Megabalanus rosa  
 C>Date: 24-Feb-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C:Accession: U01503; A26094  
 R:Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.  
 Gene 128, 251-255, 1993  
 A:Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and  
 A:Reference number: U01503; MUID:93292994; PMID:8514190  
 A:Accession: U01503  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-162 <TAK>  
 A:Cross-references: UNIPROT:Q25459; DDBJ:D13299  
 R:Muramoto, K.; Kamiya, H.  
 Biochim. Biophys. Acta 874, 285-295, 1986  
 A:Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.  
 A:Reference number: A26094  
 A:Accession: A26094  
 A:Molecule type: protein  
 A:Residues: 25-145, 'K', 147-162 <MUR>  
 A>Note: 146-Arg was also found  
 C:Comment: This galactose-binding lectin is isolated from the coelomic fluid.  
 C:Comment: This protein plays important roles in defense mechanisms and in development at  
 C:Genetics:  
 A:Introns: 22/1; 47/2; 86/3  
 C:Superfamily: tetralectin, C-type lectin homology  
 C:Keywords: hemolymph; homotetramer; lectin  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-162/Product: lectin BRA3-1 #status experimental <MAR>  
 F:26-150/Domain: C-type lectin homology <LCH>  
 F:26-39,56-150,125-142/disulfide bonds: #status experimental  
 F:157/Disulfide bonds: interchain (to 160) #status experimental  
 F:160/Disulfide bonds: interchain (to 157) #status experimental

Query Match 20.1%; Score 140; DB 1; Length 162;  
 Best Local Similarity 24.8%; Pred. No. 2.8e-07;  
 Matches 33; Conservative 27; Mismatches 51; Indels 22; Gaps 5;

QY 4 CP6G--WSSTRDYCYKPKQEWMTWASAEFSCSEQAKGHLISVETALASFYDNLVYANK 61  
 DB 26 CP6NLMQOEYDGHGYASTYQVWMDAQLACQVHGAYLATIOSOLENAFISRTVSNR 85  
 QY 62 EYTRIRYIYIGLR-----YQKQPCSSISYENLVDP-----FCFWVSQDTRLREMF 108  
 DB 86 -----LWIGLNDIDLEGHVWSNGE-ATDFTYSSNPNWENQCGVNVDTVTGQWD 138  
 QY 109 KVDCEQHSFICK 121  
 DB 139 DDDCKNRKPLCK 151

## RESULT 36

S54979  
 pancreaticitis-associated protein PAP-3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: S54979; S43438  
 R:Dusetti, N.J.; Frigerio, J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna, J.L.  
 Biochem. J. 307, 9-16, 1995  
 A:Title: Cloning, expression and chromosomal localization of the rat pancreaticitis-associ  
 A:Reference number: S54979; MUID:95234061; PMID:7717998  
 A:Accession: S54979  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-174 <DUS>  
 A:Cross-references: UNIPROT:P42854; EMBL:U09193; NID:G483931; PIDN:AA79231.1; PID:G48393  
 R:Frigerio, J.M.; Dusetti, N.J.; Garrido, P.; Dagorn, J.C.; Iovanna, J.L.  
 Biochim. Biophys. Acta 1216, 329-331, 1993  
 A:Title: The pancreaticitis associated protein III (PAP III), a new member of the PAP gene  
 A:Reference number: S43438; MUID:94060113; PMID:8241280  
 A:Accession: S43438

A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-174 <FRI>  
 A:Cross-references: GB:L20869; GB:S67496; NID:9463279; PIDN:AAA1809.1; PID:9463280  
 C:Genetics:  
 A:Introns: 26/1; 65/3; 111/3; 153/1  
 C:Superfamily: tetranelectin; C-type lectin homology  
 F:40/Domain: C-type lectin homology <LCH>

Query Match 20.1%; Score 140; DB 2; Length 174;  
 Best Local Similarity 25.5%; Pred. No. 3e-07;  
 Matches 35; Conservative 26; Mismatches 58; Indels 18; Gaps 3;

QY 2 LECPGWSSTDRYCYKPFQEMTWASAEFCSQAKGHLISVETALASFYDNLVYANK 61  
 DB 38 ISCPGRAYGXYCALFVSXKMPDADLAC-QKPSGHLVSVLSGSEASFSLSIKSSG 96  
 QY 62 EYLRITWIGLRQNGQCCSSISYF-----NLVDPFECFMSRPTLR 105  
 DB 97 N-SGQVWVIGLDPDPTLGGEPNRCGWEMSNADVNNYFNETNPSSVSGHGTLTRASGFL 155  
 QY 106 EWFKVDCEQHSFICK 122  
 DB 156 RMRNNCISELPYCKF 172

RESULT 37  
 B56829  
 albaagregin-B alpha chain - green pit viper (fragment)  
 C:Species: Trimeresurus albolabris (green pit viper)  
 C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Jul-2004  
 C/Accession: B56829  
 R:Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.; Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993  
 A:Title: Albaagregin-B and botrocetin, two snake venom proteins with highly homologous A:Accession: B56829; MUID:93221514; PMID:8466514  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-40 <YOS>  
 A:Cross-references: UNIPROT:Q9PS19  
 A:Experimental source: venom  
 A>Note: Sequence extracted from NCBI backbone (NCBIP:128751)  
 C:Superfamily: tetranelectin; C-type lectin homology  
 C:Keywords: disulfide bond; heterodimer

Query Match 20.0%; Score 139; DB 2; Length 40;  
 Best Local Similarity 57.5%; Pred. No. 7.4e-08;  
 Matches 23; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 3 ECPGWSSTDRYCYKPFQEMTWASAEFCSQAKGHL 42  
 DB 1 DCPSDWSSFRQYCYQIIKQKTMEDAFRCMDQYKAHLV 40

RESULT 38  
 LNR3  
 lectin BRA3-2 precursor - barnacle (Megabalanus rosa)  
 C:Species: Megabalanus rosa  
 C>Date: 31-Dec-1988 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: JCI504; A26094  
 R:Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T. Gene 128, 251-255, 1993  
 A:Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and A:Reference number: JCI503; MUID:93292994; PMID:8514130  
 A:Accession: JCI504  
 A:Molecule type: mRNA  
 A:Residues: 1-162 <TA>  
 A:Cross-references: UNIPROT:Q25459  
 R:Muramoto, K.; Kamiya, H. Biochim. Biophys. Acta 874, 285-295, 1986  
 A:Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.  
 A:Reference number: A26094

A:Accession: A26094  
 A:Molecule type: protein  
 A:Residues: 25-162 <MUR>  
 A>Note: 146-Arg was also found  
 C:Comment: This three galactose-binding lectin is isolated from the coelomic fluid.  
 C:Comment: This protein plays important roles in defense mechanisms and in development at C:Superfamily: tetranelectin; C-type lectin homology  
 C:Keywords: hemolymph; homotetramer; lectin  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-162/Product: lectin BRA3-2 #status experimental <MAT>  
 F:26-150/Domain: C-type lectin homology <LCH>  
 F:26-39,56-150,125-142/Disulfide bonds: #status experimental  
 F:157/Disulfide bonds: interchain (to 160) #status experimental  
 F:160/Disulfide bonds: interchain (to 157) #status experimental

Query Match 20.0%; Score 139; DB 1; Length 162;  
 Best Local Similarity 24.8%; Pred. No. 3.5e-07;  
 Matches 33; Conservative 27; Mismatches 51; Indels 22; Gaps 5;

QY 4 CPSC--WSSTDRYCYKPFQEMTWASAEFCSQAKGHLISVETALASFYDNLVYANK 61  
 DB 26 CPGLDMQYDGHCTWASTYQVRMDAQLACQTVHPGAVLATIQSLQENAFISVSNR 85  
 QY 62 EYLRITWIGLR-----VQKQPCSSISYENLVP-----PECFVSDTFLREMF 108  
 DB 86 -----LWIGLNDIDLEGHVWSNGE-ATDFTYSSNNPNNENODCGVYNDVTYTGWD 138  
 QY 109 KYDCEQHSFICK 121  
 DB 139 DDCNKNKFLCK 151

RESULT 39  
 A39808  
 proteoglycan core protein, cartilage - bovine (fragments)  
 N:Alternate names: aggrecan; aggregating cartilage proteoglycan  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 20-Mar-1992 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
 C/Accession: A34234; A27752; A39808; A27751; E29164; B27751; D27751; E27751; F27751; A:Antonsen, P.; Heinegard, D.; Oldberg, A. J. Biol. Chem. 264, 16170-16173, 1989  
 A:Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of A:Reference number: A34234; MUID:89380219; PMID:2528543  
 A:Accession: A34234  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 128-621 <ANT>  
 A:Cross-references: UNIPROT:P13608; GB:J05028  
 R:Oldberg, A.; Antonsen, P.; Heinegard, D. Biochem. J. 243, 255-259, 1987  
 A:Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a A:Reference number: A27752; MUID:87270630; PMID:3111460  
 A:Accession: A27752  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-28;59-82;131-137, 'QSER', 142-149;196-207;226-249;1137-1143;1252-1267;1274-1; R:Perin, J.P.; Bonnet, F.; Jolles, P. FEBS Lett. 206, 73-77, 1986  
 A:Title: Structural relationship between link proteins and proteoglycan monomers.  
 A:Reference number: A27751; MUID:87005253; PMID:3530809  
 A:Accession: A27751  
 A:Molecule type: protein  
 A:Residues: 29-58;74-130, 'A', 177-204;208-225 <PER>  
 R:Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.



FEBS Lett. 176, 37-42, 1984  
A>Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer  
A/Reference number: A91327; PMID:85027710; PMID:6489519  
A/Accession: E29164  
A/Molecule type: protein  
A/Residues: 1230-1249 <PE2>  
C/Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF repeats  
C/Keywords: glycoprotein  
F/8-28/Domain: link protein repeat homology (fragment) <LNK1>  
F/29-58/Domain: link protein repeat homology (fragment) <LNK2>  
F/80-146/Domain: link protein repeat homology (fragment) <LNK3>  
F/167-248/Domain: link protein repeat homology <LNK4>  
F/1130-1250/Domain: C-type lectin homology <LCH>  
F/1257-1313/Domain: complement factor H repeat homology <FHD>

Query Match 19.9%; Score 138; DB 2; Length 1340;  
Best Local Similarity 30.5%; Pred. No. 4.7e-06;  
Matches 40; Conservative 12; Mismatches 57; Indels 22; Gaps 6;

QY 4 CPGMSSTRYCYKPKQEMTWASAEFCSEQAKGHLISVETALBASFDVNLVANKY 63  
DB 1130 CEEGWTKFGCHCRHPPDATTWDAESQCRKQ--SHLSIVPEEQEFVNN---NAQ- 1182  
QY 64 LRRYIWIIGLRVQV----KGQPCSSISYENL--VDFECFMSRDTRLR-----EMFKY 110  
DB 1183 --DYQWIGLNDKTIKEDGDFRMSDGHSLQEFKRWPNQDNFATGEDCVVMIMHEKGEWMDY 1240  
QY 111 DCEQGHSPICK 121  
DB 1241 PCNYQLPFTCK 1251

## RESULT 40

phospholipase-A(2) receptor protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C/Accession: S48719  
R/Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H.  
Eur. J. Biochem. 225, 375-382, 1994  
A>Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A(2)  
A/Reference number: S48719; PMID:95010128; PMID:7925459  
A/Accession: S48719  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1487 <HIG>  
A/Cross-references: UNIPROT:Q62028; GB:D30779; NID:g1375042; PIDN:BA06443.1; PID:g69175  
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II repeat  
F/181-222/Domain: fibronectin type II repeat homology <2F1>  
F/380-503/Domain: C-type lectin homology <LCH>

Query Match 19.9%; Score 138; DB 2; Length 1487;  
Best Local Similarity 26.7%; Pred. No. 5.3e-06;  
Matches 39; Conservative 31; Mismatches 42; Indels 34; Gaps 9;

QY 4 CPGMSSTRYCYKPKQEMTWASAEFCSEQAKGHLISVETALBASFDVNLVANKY 58  
DB 957 CPGMWYFYKCKLVITIPDPRKLKWTGKQKFC--VAKGGLVSTKSELBOAFITMNL 1014  
QY 59 ANKEVLTIRYIWIIGLRVQV----KGQPC--SSISYENLV-----PFE-----CFMVS 99  
DB 1015 GQ-----TTNVTWIGLQSTNHEKWNKRPVYVSNMSPDIINIPSTTEPQKHPLCALMS 1070  
QY 100 RDTRLR---EMFKVC-EQGHSPICK 121  
DB 1071 SNENFHTGMYPDCKEGYFVCE 1096

## RESULT 41

T42630  
aggrecan - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T42630  
R/Hering, T.M.; Kollar, J.; Huynh, T.D.  
Submitted to the EMBL Data Library, September 1996  
A/Description: Complete coding sequence of bovine aggrecan: comparative structural analysis  
A/Reference number: Z22182

A/Accession: T42630  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-2327 <HER>

A/Cross-references: UNIPROT:P13608; EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AB385;  
A/Experimental source: articular chondrocytes  
C/Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF repeats  
C/Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein

Query Match 19.9%; Score 138; DB 2; Length 2327;  
Best Local Similarity 30.5%; Pred. No. 8.8e-06;  
Matches 40; Conservative 12; Mismatches 57; Indels 22; Gaps 6;

QY 4 CPGMSSTRYCYKPKQEMTWASAEFCSEQAKGHLISVETALBASFDVNLVANKY 63  
DB 2117 CEEGWTKFGCHCRHPPDATTWDAESQCRKQ--SHLSIVPEEQEFVNN---NAQ- 2169  
QY 64 LRRYIWIIGLRVQV----KGQPCSSISYENL--VDFECFMSRDTRLR-----EMFKY 110  
DB 2170 --DYQWIGLNDKTIKEDGDFRMSDGHSLQEFKRWPNQDNFATGEDCVVMIMHEKGEWMDY 2227  
QY 111 DCEQGHSPICK 121  
DB 2228 PCNYQLPFTCK 2238

## RESULT 42

ovocleidin - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 24-Oct-1998 #sequence\_revision 24-Oct-1998 #text\_change 20-Sep-1999  
C/Accession: S78596  
R/Naertholdt, D.; Andersen, S.O.  
Submitted to the Protein Sequence Database, September 1998  
A/Reference number: S78596  
A/Accession: S78596  
A/Molecule type: protein  
A/Residues: 1-142 <BAE>  
A/Experimental source: egg-shell  
C/Superfamily: tetraectin; C-type lectin homology  
C/Keywords: phosphoprotein  
F/5-16,33-138,113-110/Distulfide bonds: #status experimental  
F/61,67/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 19.6%; Score 136.5; DB 2; Length 142;  
Best Local Similarity 25.0%; Pred. No. 5.6e-07;  
Matches 35; Conservative 21; Mismatches 57; Indels 27; Gaps 4;

QY 4 CPGMSSTRYCYKPKQEMTWASAEFCSEQAKGHLISVETALBASFDVNLVANKY 61  
DB 5 CCGWVPTFGGCGGFSRSLMSRAESFCRMGPGSHLAAYNSAALRLAELNLNSRG 64  
QY 62 ---EYLTIRYIWIIGLRVQVQKQPCSSISY---ENLVDP-----ECFVWSRD 101  
DB 65 DSGGEGADRWVIGLH-----RPAGSRWSRWDGTAPASWHTAKARGRCALRDE 119  
QY 102 TRRWFVFXDCQGHSPICK 121  
DB 120 EAFTSWARPCTERNAPVCK 139

## RESULT 43

T29536  
hypothetical protein T19E7.1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29536  
R/Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of C. elegans cosmid T19E7.

A:Reference number: Z20637

A:Accession: T29536

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <PAU>

A:Cross-references: UNIPROT:Q22591; EMBL:U42843; PIDN:AAA83595.1; CESP:T19E7.1

C:Genetics:

A:Gene: CESP:T19E7.1

A:Introns: 52/3; 103/1

Query Match 19.2%; Score 133.5; DB 2; Length 178;  
Best Local Similarity 28.9%; Pred. No. 1.5e-06;

Matches 39; Conservative 15; Mismatches 58; Indels 23; Gaps 6;

QY 6 SGWSSDRCKYKFKKEMTWASAEKRCGQAKGHLTVETALFAFVNDVLYANKEYL 65

DB 52 SGWLYEDHWYKFTEDVMMIPENVC--RSMGCHLVSTIKDESENLFVHLRKKNN---- 105

QY 66 RYIWIGLRYVN-----KQOPCSSISYENLV--DPFE-----CFWVS RDTRLREMFKVD 112

DB 106 --IWIGLANKLNTDFHHYKNSDGEADYLYKMASSQRPEDVDCAYMAFHQEGCTWPDYGC 163

QY 113 EQQ--HSFTCKTRP 125

DB 164 REWLPOQFVCKLPMP 178

RESULT 44

T30273 hypothetical protein - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T30273

R:MoY, G.W.; Mendoza, L.M.; Schultz, J.R.; Swanson, W.J.; Glabe, C.G.; Vacquier, V.D.

J. Cell Biol. 133, 809-817, 1996

A:Title: The sea urchin sperm receptor for egg jelly is a modular protein with extensive

A:Reference number: Z20802; MWID:96234669; PMID:8666666

A:Accession: T30273

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1450 <MOY>

A:Cross-references: UNIPROT:Q26627; EMBL:U40833; NID:G1353652; PID:G1353653; PIDN:AA084

C:Genetics:

A:Note: REJ

Query Match 19.1%; Score 132.5; DB 2; Length 1450;  
Best Local Similarity 29.8%; Pred. No. 1.9e-05;

Matches 36; Conservative 16; Mismatches 50; Indels 19; Gaps 5;

QY 14 YCYKPKQEWMTASAEKRCGQAKGHLTVETALFAFVNDVLYANKEYLTVYIWIGR 73

DB 80 YCYLWRVDVNTQAKESCLDQKGAELASIHSAENAFV---YQ---IRRYAIGIS 132

QY 74 VQ-----NKGQPCSSISY--ENLVDPFECFVNSRDTRLREMFKVDCEQSHSICK 122

DB 133 DQYTCGVFDYADGTPVDVLSFPKKNQSETRDCVYV-KHLRVNDWGLDCKANKTSICKS 191

QY 123 T 123

DB 192 T 192

RESULT 45

I50421 aggregate precursor - chicken

N:Alternate names: cartilage chondroitin sulfate proteoglycan core protein

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072

R:Li, H.; Schwartz, N.B.; Vercel, B.M.

J. Biol. Chem. 268, 23504-23511, 1993

A:Title: CDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and

A:Reference number: A48884; MWID:94043149; PMID:8226878

A:Accession: I50421

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2109 <LIX>

A:Cross-references: UNIPROT:P07898; GB:I21913; NID:G416133; PIDN:AA019128.1; PID:G416134

R:Chandrasekaran, L.; Tanzer, M.L.

Biochem. J. 296, 885-887, 1993

A:Reference number: S39796; MWID:94107258; PMID:8280087

A:Contents: annotation, erratum

A:Accession: S39796

A:Molecule type: mRNA

A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1602, 'A',

A:Cross-references: GB:M88101

R:Chandrasekaran, L.; Tanzer, M.L.

Biochem. J. 288, 903-910, 1992

A:Title: Molecular cloning of chicken aggrecan. Structural analyses.

A:Reference number: S27356; MWID:93111968; PMID:1339285

A:Accession: S27356

A:Molecule type: mRNA

A:Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1549, 'T',

A:Cross-references: EMBL:M88101

R:Li, S.; Tanaka, T.; Koshier, R.A.; Tanzer, M.L.

Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986

A:Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglyc

A:Reference number: A25442; MWID:86259736; PMID:3460082

A:Accession: A25442

A:Molecule type: mRNA

A:Residues: 1693-1795, 'G', 1797-1855, 1894-2109 <SMI>

A:Cross-references: GB:M13993; NID:G211654; PIDN:AAA48720.1; PID:G211655

A:Experimental source: sternal cartilage

R/Tanaka, T.; Har-El, R.; Tanzer, M.L.

J. Biol. Chem. 263, 15831-15835, 1988

A:Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.

A:Reference number: A32002; MWID:85008500; PMID:3170613

A:Accession: A32002

A:Molecule type: DNA

A:Residues: 1893-1897, 'S', 1989-2022 <TAN>

A:Note: the authors translated the codon TCC for residue 1787 as Phe

R/Krueger, R.C.

J. Biol. Chem. 265, 12088-12097, 1990

A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide se

A:Reference number: I50216; MWID:90307744; PMID:1694853

A:Accession: I50216

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: PA, 1044-1559 <KRU>

A:Cross-references: GB:M38187; NID:G211685; PIDN:AAA48731.1; PID:G555441

R/Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.

J. Biol. Chem. 265, 12075-12087, 1990

A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation and

A:Reference number: A37072; MWID:90307743; PMID:2365711

A:Accession: A37072

A:Molecule type: protein

A:Residues: 998-1015, 'X', 1017-1019, 'X', 1021-1023 <KR2>

A:Note: amino end of 86k core peptide CS-A

A:Accession: B37072

A:Molecule type: protein

A:Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 <KR3>

A:Note: amino end of 75k core peptide CS-B

C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF

C:Keywords: alternative splicing

F:1-20/Domain: signal sequence #status predicted <SIS>

F:21-2109/Product: aggrecan #status predicted <MAT>

F:44-131/Domain: immunoglobulin homology <IMM>

F:166-243/Domain: link protein repeat homology <LMP>

F:264-346/Domain: link protein repeat homology <LNK1>

F:537-614/Domain: link protein repeat homology <LNK2>

F:635-716/Domain: link protein repeat homology <LNK3>

F:1859-1890/Domain: EGF homology <EGF>

F:1897-2017/Domain: C-type lectin homology <LCH>

F:2024-2080/Domain: complement factor H repeat homology <FHD>



Query Match 19.0%; Score 132; DB 1; Length 2109;  
Best Local Similarity 29.8%; Pred. No. 3.3e-05;  
Matches 39; Conservative 13; Mismatches 57; Indels 22; Gaps 6;

QY 4 CPSSGMSSTRYCYKPKQEMTWASARFCSSEAKGHLISVETALASFYDNLVANKY 63  
DB 1897 CEEGMKFGQHCYRHEERETWADASSRCREH--AHLSSITPEEQEFVNS-----H 1947  
QY 64 LRRYIWIIGL--RVON--GGQPCSSISYENL--VDFECFVMSRDLRLR-----EMFVY 110  
DB 1948 ADDYQWIGISDRAVDENFMSDGHSLQFENWRPNQDNFFPAGEDCVVMTHGEQEMNDV 2007

QY 111 DCEQOHSFICK 121  
DB 2008 PCNYHLPFICK 2018

RESULT 46  
S52781  
neurocan - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C/Accession: S52781  
R/Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.  
submitted to the EMBL Data Library, February 1995  
A/Description: Amino acid sequence of mouse neurocan and brevican and their different ex  
A/Reference number: S52781  
A/Accession: S52781  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1268 <RAU>  
A/Cross-references: UNIPROT:P55066; EMBL:X64727; NID:G758629; PIDN:CA59216.1; PID:G7586  
C/Superfamily: aggregan; C-type lectin homology; complement factor H repeat homology; EG  
F/1176-253/Domain: link protein repeat homology <LNK1>  
F/1274-355/Domain: link protein repeat homology <LNK2>  
F/1664-995/Domain: BGF homology <BGF>  
F/1040-1160/Domain: C-type lectin homology <LCH>  
F/1167-1223/Domain: complement factor H repeat homology <FHD>

Query Match 18.8%; Score 131; DB 2; Length 1268;  
Best Local Similarity 28.3%; Pred. No. 2.4e-05;  
Matches 39; Conservative 15; Mismatches 48; Indels 36; Gaps 8;

QY 4 CPSSGMSSTRYCYKPKQEMTWASARFCSSEAKGHLISVETALASFYDNLVANKY 63  
DB 1040 CDRGMHKGQHCYRFAHRRAMEDARDERRA--GHLISVHSPBEHKTINSFGHNS-- 1095  
QY 64 LRRYIWIIGL-----VONKGQPCSSISYEN--LVDPF-----EC-FMVSRDTR 103  
DB 1096 -----WIGLNDRTVERDPQMTDNTG-----LOYENRERQPDNFFAGGEDCVVMVAHES- 1144

QY 104 LREWFVDCQOHSFICK 121  
DB 1145 -GRMNDVPCNYLPLVYCK 1161

RESULT 47  
A26697  
echinoidin - sea urchin (Anthocidaris crassispina)  
C/Species: Anthocidaris crassispina  
C/Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
C/Accession: A26697  
R/Rigge, Y.; Ixai, A.; Takahashi, K.  
J. Biol. Chem. 262, 6197-6203, 1987  
A/Title: The complete amino acid sequence of echinoidin, a lectin from the coelomic fluid  
A/Reference number: A26697; MID:87194838; PMID:3571253  
A/Accession: A26697  
A/Molecule type: protein  
A/Residues: 1-147 <SIG>  
A/Cross-references: UNIPROT:P06027  
C/Superfamily: tetralectin; C-type lectin homology  
F/3-141/Domain: C-type lectin homology <LCH>

F/3-14,31-141,116-132/Disulfide bonds: #status predicted

Query Match 18.7%; Score 130; DB 2; Length 147;  
Best Local Similarity 26.2%; Pred. No. 2.8e-06;  
Matches 37; Conservative 24; Mismatches 56; Indels 24; Gaps 7;

QY 4 CPSSGMSSTRYCYKPKQEMTWASARFCSSEAKGHLISVETALASFYDNLVANKY 55  
DB 3 CPTFMTSPGNCYRFFAVSLTWABEQFCQSPFSVRGIDISIGHLISHSFTEQNFVYH 62  
QY 56 VL-YANKELVTRVYIWIIGL-RVQ-----NKGQPCSSISY-----ENVDPFECFVMSRD 101  
DB 63 YFETSTKDDTTPPEMMLGFNDRTTEGNFQMTDSFNDFTAWGNSPDNYSGSDCTQWNG 122

QY 102 TLREWFVDCQOHSFICK 121  
DB 123 AGL-NWIDLPCSTRHYLICK 142

RESULT 48  
S28764  
neurocan precursor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Nov-1993 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C/Accession: S28764  
R/Rauch, U.; Karchlikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.  
J. Biol. Chem. 267, 19536-19547, 1992  
A/Title: Cloning and primary structure of neurocan, a developmentally regulated, aggregat  
A/Reference number: S28764; MID:92406907; PMID:1326557  
A/Accession: S28764  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1257 <RAU>  
A/Cross-references: UNIPROT:P55067; EMBL:M97161; NID:G205649; PIDN:AAC37679.1; PID:G2056  
C/Superfamily: aggregan; C-type lectin homology; complement factor H repeat homology; EG  
C/Keywords: chondroitin sulfate proteoglycan; glycoprotein  
F/1-22/Domain: signal sequence #status predicted <Sig>  
F/23-1257/Domain: link protein repeat homology <LNK1>  
F/176-253/Domain: link protein repeat homology <LNK2>  
F/274-355/Domain: link protein repeat homology <LNK2>  
F/364-366/Region: cell attachment (R-G-D) motif  
F/953-984/Domain: BGF homology <BGF>  
F/1029-1149/Domain: C-type lectin homology <LCH>  
F/1156-1212/Domain: complement factor H repeat homology <FHD>  
F/121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted  
F/44/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

Query Match 18.7%; Score 130; DB 2; Length 1257;  
Best Local Similarity 28.3%; Pred. No. 3e-05;  
Matches 39; Conservative 14; Mismatches 49; Indels 36; Gaps 8;

QY 4 CPSSGMSSTRYCYKPKQEMTWASARFCSSEAKGHLISVETALASFYDNLVANKY 63  
DB 1029 CDRGMHKGQHCYRFAHRRAMEDARDERRA--GHLISVHSPBEHKTINSFGHNS-- 1084  
QY 64 LRRYIWIIGL-----VONKGQPCSSISYEN--LVDPF-----EC-FMVSRDTR 103  
DB 1085 -----WIGLNDRTVERDPQMTDNTG-----LOYENRERQPDNFFAGGEDCVVMVAHES- 1133

QY 104 LREWFVDCQOHSFICK 121  
DB 1134 -GRMNDVPCNYLPLVYCK 1150

RESULT 49  
I83377  
regenerating protein III (reg III) - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C/Accession: I60296; I83377  
R/Suzuki, Y.; Yonekura, H.; Watanabe, T.; Unno, M.; Morizumi, S.; Miyashita, H.; Okamoto  
Gene 144, 315-316, 1994  
A/Title: Structure and expression of a novel rat RegIII gene.

A:Reference number: I60296; MWID:94314238; PMID:8039722  
A:Accession: I60296  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-174 <RES>  
A:Cross-references: UNIPROT:P35231; GB:D23676; NID:g471157; PIDN:BA04904.1; PID:g471158  
A:Accession: I83377  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-174 <RE2>  
A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160  
A:Gene: RegIII  
A:Introns: 25/1; 64/3; 110/3; 153/1  
C:Superfamily: cetranelectin; C-type lectin homology  
F:39-170/Domain: C-type lectin homology <LCH>

Query Match 18.5%; Score 128.5; DB 2; Length 174;  
Best Local Similarity 25.4%; Pred. No. 4.8e-06;  
Matches 36; Conservative 21; Mismatches 54; Indels 31; Gaps 4;

QY 4 CPFGMSSTDRYCKPKEKMTWASARFSGEAKGCHLSVETALFASFDVNLVANKY 63  
DB 39 CPFGSKAYRSYCYTLVTTLSKMPQADIAC-QKRPSGHLVSLSGEASFVS-LVTGRVN 96  
QY 64 LTRFYIWIGLRVONKQ-----PCSSISYENLVDPFECFMSR 100  
DB 97 NNODIWIIGLHDPFMGQOPNGGWMNSDVLNTLNMNDGPBSTVNRGN-----CGSLTA 150  
QY 101 DTRLREWFKVDCEQHSFICKF 122  
DB 151 TSEFLKWKGDHHCDELPEVCKF 172

## RESULT 50

T42710  
mannose receptor, macrophage - mouse  
N:Alternate names: lambda lectin; phospholipase A2 receptor  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T42710  
R:Wu, K.; Yuan, J.; Lasky, L.A.  
J. Biol. Chem. 271, 21323-21330, 1996  
A:Title: Characterization of a novel member of the macrophage mannose receptor type C 1e  
A:Reference number: 222235; MWID:6355501; PMID:8702911  
A:Accession: T42710  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1479 <WUK>  
A:Cross-references: UNIPROT:Q64449; EMBL:U56734; NID:g1336073; PID:g1336074; PIDN:AAC527  
C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re  
C:Keywords: membrane protein; receptor  
F:186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 18.3%; Score 127.5; DB 2; Length 1479;  
Best Local Similarity 29.1%; Pred. No. 6.6e-05;  
Matches 44; Conservative 16; Mismatches 54; Indels 37; Gaps 8;

QY 4 CPFGMSSTD-RYCKRFKQE-----MTWASARFSGEAKGCHLSVETALFASFDVNV 56  
DB 668 CPQGWSDPKLRHCYKVFSSRIQEKSWIQALGVCRE-LGAQLSLASVEEHFVAM 725  
QY 57 LYANK-----EYLTRFYIWIGLRVONKQPCSSISY---ENLVDPFECFMSR----- 100  
DB 726 L--NKITGESPEHSHQHWIIGL---NRDPRRGHSWRMSDGLGFSYHNFPARSRHDD 780  
QY 101 -----DTRLREWFKVDCEQHSFICKFTR 124  
DB 781 IRGCAVLDSLQWVPMQCOTOLDWICKIPR 811

Search completed: May 2, 2005, 16:02:20  
Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:06 ; Search time 68 Seconds  
(without alignments)  
948,853 Million cell updates/sec

Title: US-10-749-387-1

Perfect score: 695  
Sequence: 1 DIECPGSGWSTDRYCYKPK.....WFKVDCQGHSPICKETPR 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 65 summaries

Database :  
1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	94.7	127	1	CHBA_CROHO
2	371	53.4	155	2	Q9DEA2
3	364	52.4	155	2	Q8JIV6
4	360.5	51.9	158	2	Q719L9
5	358.5	51.6	156	2	Q71R06
6	358.5	51.6	156	2	Q71R07
7	357.5	51.4	133	1	RHCA_AGRKH
8	357	51.4	157	1	MMHA_AGRHA
9	353.5	50.9	156	2	Q71R04
10	351.5	50.6	156	2	Q71R02
11	335	48.2	142	2	Q9PSM6
12	332.5	47.8	129	2	Q71Z71
13	326.5	47.0	131	1	ABAI_TRIAB
14	320.5	46.1	129	1	RHCA_AGRKH
15	314.5	45.3	132	2	ABBA_TRIAB
16	314.5	45.3	158	2	Q8AYAS
17	311	44.7	133	1	BOTA_BOTJA
18	310.5	44.7	158	2	Q8AV97
19	309.5	44.5	158	2	Q8UVC6
20	309.5	44.5	158	2	Q71R01
21	306.5	44.1	134	1	ABBA_TRIAB
22	304.5	43.8	154	2	Q8JIV9
23	304.5	43.8	154	2	Q9YGN5
24	302.5	43.5	146	2	Q98UJ0
25	302.5	43.5	152	1	IXA_TRIPL
26	300.5	43.2	158	2	Q8JGT7
27	300.5	43.2	158	2	Q6TRH0
28	293.5	42.2	158	1	CVXB_CRODU
29	292.5	42.1	152	2	Q9D539
30	288.5	41.5	152	2	Q8JTW0
31	288.5	41.5	152	2	Q9DEF9

32	288	41.4	136	2	Q91841	Q91841 agkistrodon
33	287.5	41.4	152	2	Q918M1	Q918M1 agkistrodon
34	275.5	39.6	152	2	Q71R44	Q71R44 trimeresuru
35	273.5	39.4	158	2	Q696W1	Q696W1 vipera lebe
36	268.5	38.6	121	2	Q75ZV0	Q75ZV0 agkistrodon
37	265.5	38.2	131	2	Q77248	Q77248 echis carin
38	262	37.7	133	2	Q677B6	Q677B6 echis carin
39	256.5	36.9	156	1	ECHA_ECHCA	ECHA_ECHCA echis carin
40	255.5	36.8	146	2	Q8AY44	Q8AY44 agkistrodon
41	252.5	36.3	123	1	ABBA_TRIAB	ABBA_TRIAB trimeresuru
42	251.5	36.2	152	2	Q6X5T3	Q6X5T3 bits ariet
43	249.5	35.9	146	2	Q91AM0	Q91AM0 agkistrodon
44	249.5	35.9	148	1	CVXB_CRODU	CVXB_CRODU crocatus du
45	248.5	35.8	146	2	Q8JIV1	Q8JIV1 agkistrodon
46	246.5	35.5	148	2	Q71R08	Q71R08 trimeresuru
47	244	35.1	157	2	Q6T7B5	Q6T7B5 echis gabon
48	243.5	35.0	157	2	Q77201	Q77201 echis mult
49	242.5	34.9	131	2	Q71ZK5	Q71ZK5 bits ariet
50	242.5	34.9	148	2	Q71R09	Q71R09 trimeresuru
51	237.5	34.2	131	2	Q9PSM9	Q9PSM9 echis carin
52	225.5	32.4	146	2	Q91840	Q91840 agkistrodon
53	219.5	31.6	148	2	Q8AV98	Q8AV98 trimeresuru
54	218.5	31.4	123	2	Q71Z72	Q71Z72 vipera russ
55	218.5	31.4	148	2	Q71R08	Q71R08 crocatus du
56	217.5	31.3	146	2	Q77045	Q77045 vipera lebe
57	217.5	31.3	148	2	Q6X5T2	Q6X5T2 bits ariet
58	217	31.2	149	2	Q8UVC7	Q8UVC7 agkistrodon
59	215.5	31.0	124	2	Q90WL9	Q90WL9 agkistrodon
60	215.5	31.0	146	2	Q8UVC6	Q8UVC6 trimeresuru
61	215.5	31.0	148	2	Q6X5T0	Q6X5T0 echis ocell
62	214	30.8	149	2	Q8AY43	Q8AY43 agkistrodon
63	212.5	30.6	148	2	Q6X5S3	Q6X5S3 echis pyram
64	212.5	30.6	148	2	Q6X5S7	Q6X5S7 echis ocell
65	212.5	30.6	148	2	Q6X5S8	Q6X5S8 echis carin

## ALIGNMENTS

RESULT 1	CHBA_CROHO	STANDARD;	PRT;	127 AA.
AC	P81508			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	CH-B alpha subunit.			
OS	Crotalus horridus horridus (Timber rattlesnake).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Viperidae; Crotalinae; Crotalus.			
OK	NCBI_TaxID=8747;			
RN	[1]			
RP	SEQUENCE.			
RC	TRISUE-Venom;			
RX	MEDLINE=96420502; PubMed=8823201; DOI=10.1021/b1960704e;			
RA	Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,			
RA	Smith A.I., Lopez J.A., Bernd M.C.;			
RT	"Binding of a novel 50-kilodalton albaaggregin from Trimeresurus			
RT	albobratis and related viper venom proteins to the platelet membrane			
RT	glycoprotein Ib-IX-V complex. Effect on platelet aggregation and			
RT	glycoprotein Ib-mediated platelet activation.";			
RL	Biochemistry 35:12629-12639(1996).			
CC	-I- FUNCTION: Binds to platelet GPIIb/III receptor system, inhibits vWF			
CC	binding, and stimulates aggregation.			
CC	-I- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.			
CC	-I- SIMILARITY: Contains 1 C-type lectin family domain.			
DR	HSSP: P22030, 110K.			
DR	InterPro: IPR002353; AntifreezeZell.			
DR	InterPro: IPR001304; Lectin_C.			
DR	Pfam: PF00059; Lectin_C; 1.			
DR	PRINTS: PR00356; ANTI-FREEZEZELL.			

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DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS0041; C TYPE LECTIN 2; 1.
KM Direct protein sequencing; Lectin.
FT DOMAIN 11 121 C-type lectin.
FT DISULFID 4 15 By similarity.
FT DISULFID 32 120 By similarity.
FT DISULFID 81 81 Interchain (with C-92 in beta chain)
FT (potential).
FT DISULFID 95 112 By similarity.
SQ SEQUENCE 127 AA; 15162 MW; B5DA100D383E347 CRC64;

Query Match 94.7%; Score 658; DB 1; Length 127;
Best Local Similarity 95.2%; Pred. No. 1.1e-61;
Matches 120; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIECPGMSSTRDYCYKPFKQEMTWASAEFCSQAKGHHLSVETALASFDVNLVANK 60
DB 1 DIECPGMSSTRDYCYKPFKQEMTWASAEFCSQAKGHHLSVETALASFDVNLVANK 60
QY 61 KEVLTYYIWIGLRVONKQGPCSSISYENLVDPFCEFMVSRDTRLRMFVDCSQOHSFTIC 120
DB 61 KEVLTYYIWIGLRVONKQGPCSSISYENLVDPFCEFMVSRDTRLRMFVDCSQOHSFTIC 120
QY 121 KFTRRP 126
DB 121 KFTRRP 126

RESULT 2
QYDEA2 PRELIMINARY; PRT; 155 AA.
AC Q9DEA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Agkicetin alpha subunit precursor.
GN Name=GP1BA1;
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxId=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Y.L., Hong T.M., Chang T., Tsai I.H.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF102801; AAG42040.1; -.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITTSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS0041; C TYPE LECTIN 2; 1.
KM Signal.
FT SIGNAL 1 23 potential.
FT CHAIN 24 155 agkicetin alpha subunit.
SQ SEQUENCE 155 AA; 17798 MW; 92B40281A797AADC CRC64;

Query Match 53.4%; Score 371; DB 2; Length 155;
Best Local Similarity 53.4%; Pred. No. 3.3e-31;
Matches 71; Conservative 20; Mismatches 32; Indels 10; Gaps 3;

QY 3 ECPGMSSTRDYCYKPFKQEMTWASAEFCSQAKGHHLSVETALASFDVNLVANK 62
DB 24 DCLPGMSSTRDYCYKPFKLTKTWEDAEFCTEQANGCHLVSPSAREADFFVAGVLSENIK 83
QY 63 YLTYYIWIGLRVONKQGPCSSISYENLVDPF--ECFMVSRDTRLRMFVDC 113
DB 84 -IKPYWIGLRVONKQGPCSSISYENLVDPF--ECFMVSRDTRLRMFVDC 142

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QY 114 QOHSFICKETRRP 126
DB 143 LKHVFMCKYLKRP 155

RESULT 3
QYDEA2 PRELIMINARY; PRT; 155 AA.
AC Q9DEA2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Antithrombin A-A-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxId=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091762; AAM22790.1; -.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITTSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS0041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 155 AA; 17715 MW; 6E55C95E97A1D7 CRC64;

Query Match 52.4%; Score 364; DB 2; Length 155;
Best Local Similarity 52.6%; Pred. No. 1.8e-30;
Matches 70; Conservative 20; Mismatches 33; Indels 10; Gaps 3;

QY 3 ECPGMSSTRDYCYKPFKQEMTWASAEFCSQAKGHHLSVETALASFDVNLVANK 62
DB 24 DCLPGMSSTRDYCYKPFKLTKTWEDAEFCTEQANGCHLVSPSAREADFFVAGVLSENIK 83
QY 63 YLTYYIWIGLRVONKQGPCSSISYENLVDPF--ECFMVSRDTRLRMFVDC 113
DB 84 -IKPYWIGLRVONKQGPCSSISYENLVDPF--ECFMVSRDTRLRMFVDC 142
QY 114 QOHSFICKETRRP 126
DB 143 LKHVFMCKYLKRP 155

RESULT 4
QYDEA2 PRELIMINARY; PRT; 158 AA.
AC Q719L9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Crocotoxin-1.
OS Crocotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crocotalus.
OX NCBI_TaxId=8732;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Venom gland;
RA Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF541883; AAQ11364.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.

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DR InterPro: IPR003990; Pancreatitis_ac.
DR Pfam: PF00059; Lectin C; 1.
DR PRINTS: PR01504; PNCREATITISAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 158 AA; 18195 MW; 3FA3B316469D1DE9 CRC64;

Query Match: 51.9%; Score 360.5; DB 2; Length 158;
Best Local Similarity 47.4%; Pred. No. 4,4e-30;
Matches 64; Conservative 27; Mismatches 35; Indels 9; Gaps 2.

QY 1 DLECPGSSSTDYCYKPKFQKEMTWASAEKFCSEBQAKGHLISVETALAEAFVDNVLTYAN 60
Db 24 DFDCEGSAIDQYRYRIVKQLKTWEDAEWFTCTKQAKGHLISVESAAGADFAQVLVEN 83
QY 61 KEYLTRYIWIIGLRVONKQPC-----SSISYENLVDPF--ECFVWSRDTRLREMFVYD 111
Db 84 IKONKYVWIIGLRVONKQPCSTKMSDSSVYENLVLSYSKKCGAKKETEFLQWNTD 143
QY 112 CEQGHSPICKFTPR 126
Db 144 CEKXNLFVCKEPPQR 158

RESULT 5
Q7IR06 PRELIMINARY; PRT; 156 AA.
Q7IR06
AC Q7IR06;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS SteAggRegin-B alpha chain-2.
OS Trimeresurus steinegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
NC NCBI_TaxID=39682;
RN 11
RX SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Lee W.-H., Liu H., Zhang Y.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF34919; AAQ1516.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro: IPR001304; Lectin C.
DR InterPro: IPR003990; Pancreatitis_ac.
DR Pfam: PF00059; Lectin C; 1.
DR PRINTS: PR01504; PNCREATITISAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 156 AA; 17984 MW; C08E54F955369DFD CRC64;

Query Match: 51.6%; Score 358.5; DB 2; Length 156;
Best Local Similarity 52.2%; Pred. No. 7e-30;
Matches 70; Conservative 18; Mismatches 35; Indels 11; Gaps 4.

QY 3 ECPGMSSTDYCYKPKFQKEMTWASAEKFCSEBQAKGHLISVETALAEAFVDNVLTYANKE 62
Db 24 DCEPDMSSEFKQYQIQLKTWEDAEKFCVDQVGAALVSIESTREYVFAAQQSENVK 83
QY 63 YLTREY-IWIGLRVONKQPC-----SSISYENLVDPF--ECFVWSRDTRLREMFVYD 112
Db 84 -TTKYDWIIGLSVYNNKGGQCSSEMSDSSVYENLVKLSKKCFVLKKGTFRKKNVAC 142
QY 113 EQGHSFICKFTPR 126
Db 143 EOKHLFMCKFLRPR 156

RESULT 6
Q7IR07

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ID	Q1:R07	PRELIMINARY;	PRT;	156 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	stejagreglin-B alpha chain-1.			
OS	Trimeresurus stejnegeri (Chinese green tree viper).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Leiodontia; Squamata; Scleroglossa; Serpentes; Colubroidae;			
CC	Viperidae; Crotalinae; Trimeresurus.			
OX	NCBI_TaxID=39682;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Lee W.-H., Liu H., Zhang Y.;			
RL	Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF354918; AAQ15160.1; -			
DR	GO; GO:0005529; F: sugar binding; IEA.			
DR	InterPro; IPR001304; Lectin_C.			
DR	InterPro; IPR003900; Pancreatic_ac.			
DR	Pfam; PF00059; Lectin_C; 1.			
DR	PRINTS; PRO1504; PNCREATITAP.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C TYPE LECTIN 1; 1.			
DR	PROSITE; PS50041; C TYPE LECTIN 2; 1.			
DR	SEQUENCE 156 AA; 17924 MW; 4AFA11F9A167D586 CRC64;			
SO	SEQUENCE			
QY	Query Match			
Db	Best Local Similarity 51.6%; Score 358.5; DB 2; Length 156;			
Matches	70; Conservative 16; Mismatches 35; Indels 11; Gaps 4;			
QY	3 ECPGSGSTDRYCYKPKROKMTWASARFCSEQAKGGHLISVEFALDEASFDVNLVYANKE 62			
Db	24 DCPEDMSSEFYQYCIQIKLKTWEDARFCDDQYKGAHLVISIESYREAVFPAQOLSENVK 83			
QY	63 YLTGY-TWIGLRVGNKQOPC-----SSTSYENLNDPF--ECPMWSRDTFLREMPKYDC 112			
Db	84 -TTYIDWVIGLSVNVKQCCSSSEWSDSSVSYENLVKPLSKCFVLKKGTFFRPMFNVAC 142			
QY	113 ECHSFPICKFTPR 126			
Db	143 EQKHLFWCKFLRPR 156			
RESULT 7				
RHCA_AGRKH				
ID	RHCA_AGRKH	STANDARD;	PRT;	133 AA.
AC	P81357;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Rhodocetin alpha subunit.			
OS	Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Leiodontia; Squamata; Scleroglossa; Serpentes; Colubroidae;			
CC	Viperidae; Crotalinae; Calloselasma.			
OX	NCBI_TaxID=8717;			
RN	[1]			
RP	SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.			
RC	TISSUE=Venom.			
RX	MEDLINE=9930398; PubMed=10360956; DOI=10.1021/bj982132z;			
RA	Wang R., Kim R.M., Chung M.C.M.;			
RT	"Rhodocetin, a novel platelet aggregation inhibitor from the venom of			
RT	Calloselasma rhodostoma (Malayan pit viper): synergistic and			
RT	noncovalent interaction between its subunits.";			
RL	Biochemistry 38:7584-7593(1999).			
CC	-1- FUNCTION: A potent inhibitor of collagen-induced platelet			
CC	aggregation. Individually, neither subunit inhibits platelet			
CC	aggregation. Both subunits are essential.			
CC	-1- SUBUNIT: Heterodimer of one alpha and one beta subunit held			
CC	together by noncovalent interactions rather than by intersubunit			
CC	disulfide bridges.			
CC	-1- SUBCELLULAR LOCATION: Secreted			

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CC -1- MASS SPECTROMETRY: MW=15955.90; MW_ERR=1.44; METHOD=Electrospray;
CC RANGE=1-133; NOTE=Ref.1.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSSP; P22030; 11UK.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Direct protein sequencing; Lectin.
FT DOMAIN 1 129 C-type lectin.
FT DISULFID 2 13 By similarity.
FT DISULFID 30 127 By similarity.
FT DISULFID 102 119 By similarity.
SQ SEQUENCE 133 AA; 15962 MW; 386BAC519DFC674D CRC64;

Query Match 51.4%; Score 357.5; DB 1; Length 133;
Best Local Similarity 49.6%; Pred. No. 7.5e-30;
Matches 66; Conservative 22; Mismatches 36; Indels 9; Gaps 2;

QY 3 ECPGSGSITDRYCYKPKFQKQMTWASAEFCSEQAKGHLISVETALEASFDVNLVYANKE 62
DB 1 DCPDGMSSITKSYCYRFRPKKKTWEAEKCTEOKKAHLVSMENRLEAVFDMVMENRFE 60
QY 63 YLTRYIWIIGLRVONKQPC-----SSISYENVLPD--ECFMWSRDTRLREMFKVDCE 113
DB 61 NKIYRWISGKTIENKQQRNLSEWSDSSISYENVLPYPMKCKPLMDHGSLPRMTADCE 120
QY 114 QCHSPICKETRRR 126
DB 121 EKNVFWCKFLPR 133

RESULT 8
MMHA_AKGHA STANDARD; PRT; 157 AA.
ID MMHA_AKGHA
AC Q9YGG9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mamushigin alpha chain precursor.
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffi).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA MEDLINE=98319530; PubMed=9657448;
RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA Suzuki M., Matsui T., Titiari K., Yoshiooka A.;
RT "The CDNA cloning and molecular characterization of a snake venom
RT platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
RT halys blomhoffi venom."
RT Thromb. Haemost. 79:1199-1207(1998).
RL FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet
CC aggregation at low-shear stress. At high-shear stress, aggregation
CC is inhibited.
CC -1- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=16825; MW_ERR=2.7; METHOD=Electrospray;
CC RANGE=22-157; NOTE=Ref.1.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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DR EMBL; AB019615; BA034424.1; -.
DR HSSP; P23806; 1034.
DR GO; GO:0005576; C:extracellular; IC.
DR GO; GO:0007596; P:blood coagulation; IDA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancratia_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSPAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Blood coagulation; Direct protein sequencing; Lectin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 157 Mamushigin alpha chain.
FT DOMAIN 34 152 C-type lectin.
FT DISULFID 27 38 By similarity.
FT DISULFID 55 151 By similarity.
FT DISULFID 103 103 Interchain (with C-98 in beta chain) (By
FT similarity).
SQ SEQUENCE 157 AA; 18333 MW; 47DAA17891CE1865 CRC64;

Query Match 51.4%; Score 357; DB 1; Length 157;
Best Local Similarity 50.4%; Pred. No. 1e-29;
Matches 68; Conservative 24; Mismatches 33; Indels 10; Gaps 3;

QY 1 DLECPGSGSITDRYCYKPKFQKQMTWASAEFCSEQAKGHLISVETALEASFDVNLVYANKE 60
DB 24 DSDCPDGMSSITKSYCYRFRPKKKTWEAEKCTEOKKAHLVSMENRLEAVFDMVMENRFE 83
QY 61 KEYLTRYIWIIGLRVONKQPC-----SSISYENVLPD--ECFMWSRDTRLREMFKVD 111
DB 84 IK-KTDYVWIGLTVQNEEQCKSRWSDRSSYENVLPYPMKCKPLMDHGSLPRMTADCE 142
QY 112 CEQCHSPICKETRRR 126
DB 143 CGQKTAFWCKFLPR 157

RESULT 9
Q71RQ4 PRELIMINARY; PRT; 156 AA.
ID Q71RQ4
AC Q71RQ4;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Stejagregin-B alpha chain-3.
OS Trimeresurus stejageri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Lee W.-H., Liu H., Zhang Y.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL; AF354921; AA015163.1; -.
RA EMBL; AF354922; AA015164.1; -.
RA EMBL; AF354920; AA015162.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancratia_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSPAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 156 AA; 17972 MW; C09FB50944D76FDF CRC64;

Query Match 50.9%; Score 353.5; DB 2; Length 156;
Best Local Similarity 51.5%; Pred. No. 2.4e-29;
Matches 69; Conservative 18; Mismatches 36; Indels 11; Gaps 4;

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QY 3 ECPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 62
DB 24 DCPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 83
QY 63 YLTRV-ITWGLAVONKGPC-----SSISYENLVDPF--EGFWSRSDRLREMKVDC 112
DB 84 -TTKYDVMWGLSVNKGQCCSSSEWSDGSSVSENLVPLSKKCFVLKKGTEFRKFWNVAC 142
QY 113 EOOHSPICKETPR 126
DB 143 EOKHLFMCKFLRPR 156

RESULT 10
Q71RQ2 PRELIMINARY; PRT; 156 AA.
AC Q71RQ2;
DB 05-JUL-2004 (TREMBLrel). 27, Created)
DB 05-JUL-2004 (TREMBLrel). 27, Last sequence update)
DB 05-JUL-2004 (TREMBLrel). 27, Last annotation update)
DB Stejagregin-B alpha chain-4.
DB Trimeresurus stejnegeri (Chinese green tree viper).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
DB Viperidae; Crotalinae; Trimeresurus.
DB NCBI_TaxID=39682;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Lee W.-H., Liu H., Zhang Y.,
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354923; AA015165.1; -.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatic_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITTSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 156 AA; 17824 MW; 4AAFD0894167D58F CRC64;

Query Match 50.6%; Score 351.5; DB 2; Length 156;
Best Local Similarity 51.5%; Pred. No. 3.9e-29;
Matches 69; Conservative 18; Mismatches 36; Indels 11; Gaps 4;

QY 3 ECPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 62
DB 24 DCPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 83
QY 63 YLTRV-ITWGLAVONKGPC-----SSISYENLVDPF--EGFWSRSDRLREMKVDC 112
DB 84 -TTKYDVMWGLSVNKGQCCSSSEWSDGSSVSENLVPLSKKCFVLKKGTEFRKFWNVAC 142
QY 113 EOOHSPICKETPR 126
DB 143 EOKHLFMCKFLRPR 156

RESULT 11
Q9PSM6 PRELIMINARY; PRT; 142 AA.
AC Q9PSM6;
DB 01-MAY-2000 (TREMBLrel). 13, Created)
DB 01-MAY-2000 (TREMBLrel). 13, Last sequence update)
DB 01-OCT-2003 (TREMBLrel). 25, Last annotation update)
DB Platelet glycoprotein IB-binding protein alpha subunit, GPIIb-IIIa
DB subunit.
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
DB Viperidae; Crotalinae; Bothrops.

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OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX MEDLINE=96209990; PubMed=8631868; DOI=10.1074/jbc.271.18.10635;
RA Kawasaki T., Fujimura Y., Usami Y., Suzuki M., Mura S., Sakurai Y.,
RA Makita K., Tanuchi Y., Hirano K., Ritani K.;
RT "Complete amino acid sequence and identification of the platelet
RT glycoprotein Ib-binding site of Jararaca GP1b-BP, a snake venom
RT protein isolated from Bothrops jararaca.";
RL J. Biol. Chem. 271:10635-10639(1996).
DR HSP; P22029; 1FVJ.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 142 AA; 16720 MW; E28FDEB8F922004 CRC64;

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Query Match 48.2%; Score 335; DB 2; Length 142;
Best Local Similarity 47.1%; Pred. No. 1.9e-27;
Matches 65; Conservative 23; Mismatches 36; Indels 14; Gaps 3;

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QY 3 ECPGWSSTDRYCYKPFKQEMTW-----ASAEKFCSEQAKGHLISVETALASFDVNL 57
DB 5 ECPGWSSTDRYCYKPFKQEMTW-----ASAEKFCSEQAKGHLISVETALASFDVNL 64
QY 58 YANKEVLTWYIGLVONKGPC-----SSISYENLV--DPECFWVSRLRLREMF 108
DB 65 APVIGSKYTWYIGLVONKGPC-----SSISYENLV--DPECFWVSRLRLREMF 124
QY 109 KYDCEQSHSFKETPR 126
DB 125 NIDCVGNPFVKETPR 142

RESULT 12
Q7LZ71 PRELIMINARY; PRT; 129 AA.
AC Q7LZ71;
DB 01-MAR-2004 (TREMBLrel). 26, Created)
DB 01-MAR-2004 (TREMBLrel). 26, Last sequence update)
DB 01-MAR-2004 (TREMBLrel). 26, Last annotation update)
DB Coagulation factor IX-binding protein A chain.
DB Trimeresurus flavoviridis (Habu) (Procolobrops flavoviridis).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
DB Viperidae; Crotalinae; Trimeresurus.
DB NCBI_TaxID=88087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96318509; PubMed=8749314;
RA Aboda H., Ishikawa M., Yoshihara E., Sekiya F., Morita T.;
RT "Blood coagulation factor IX-binding protein from the venom of
RT Trimeresurus flavoviridis: purification and characterization.";
RL J. Biochem. 118:965-973(1995).
DR PIR; J04329; J04329.
DR HSP; P23806; IJ34.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 129 AA; 14640 MW; 225F3C7D841D6C76 CRC64;

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Query Match 47.8%; Score 332.5; DB 2; Length 129;
Best Local Similarity 47.7%; Pred. No. 3.2e-27;
Matches 61; Conservative 23; Mismatches 35; Indels 9; Gaps 2;

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QY 3 ECPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 62
DB 1 DCPGWSSTDRYCYKPFKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVANK 60

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OY 63 YLTRYIWMIGLRVNGKQPC-----SSISYENLVDPFE--CFMWSRDRTRLEMPKVDK 113  
 DB 61 NTKSYWIMIGLRVNGKQPCSSSEWSDSSSYENWIEASKECTGLGKETGFRKWNVYCG 120  
 OY 114 OOHSPICK 121  
 DB 121 QONPFVCE 128

RESULT 13  
 ID ABBA TRIAB STANDARD; PRT; 131 AA.

AC P8111;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Albogreggin A subunit 1.  
 OS Trimeresurus albolabris (White-lipped pit viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 OX NCBI\_Taxid=8765;

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 DR HSSP; P23806; J134.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00611; C\_TYPE\_LLECTIN\_2; 1.  
 KW Direct protein sequencing; Lectin.  
 FT DOMAIN 1 131 C-type lectin.  
 FT DISULFID 2 13 By similarity.  
 FT DISULFID 30 127 By similarity.  
 FT DISULFID 102 119 By similarity.  
 SQ SEQUENCE 131 AA; 15427 MW; B3569F5BF91F6624 CRC64;

Query Match 47.0%; Score 326.5; DB 1; Length 131;  
 Best Local Similarity 46.6%; Pred. No. 1.4e-26;  
 Matches 61; Conservative 20; Mismatches 41; Indels 9; Gaps 2;

OY 3 ECPGSGSSTDRYCYKPFKQEMTWASARFCSEQAKGHLISVETALASFDVNLVYANKE 62  
 DB 1 DCPSPDSSSDYQCYRVFKRIQTWEDAEKFCSEQANDGHVLSIAEADPVLQVSENIR 60  
 OY 63 YLTRYIWMIGLRVNGKQPC-----SSISYENLVDPFE--CFMWSRDRTRLEMPKVDK 113  
 DB 61 SEKHVWIGLRVNGKQPCSSSEWSDSSSYENWIEASKECTGLGKETGFRKWNVYCG 120  
 OY 114 OOHSPICK 124  
 DB 121 HEYPFVCKFXR 131

RESULT 14  
 ID RHCB AGKRH STANDARD; PRT; 129 AA.  
 AC P81358;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Rhodocetin beta subunit.  
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Calloselasma.  
 OX NCBI\_Taxid=8717;

CC -1- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.  
 CC -1- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=15184.53; MW\_ERR=2.74; METHOD=Electrospray;  
 CC RANGE=1-129; NOTE=Ref.1.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 DR HSSP; P22030; I10K.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00611; C\_TYPE\_LLECTIN\_2; 1.  
 KW Direct protein sequencing; Lectin.  
 FT DOMAIN 3 125 C-type lectin.  
 FT DISULFID 4 15 By similarity.  
 FT DISULFID 98 115 By similarity.  
 SQ SEQUENCE 129 AA; 15190 MW; EFAB318FAC8070AE CRC64;

Query Match 46.1%; Score 320.5; DB 1; Length 129;  
 Best Local Similarity 44.5%; Pred. No. 6e-26;  
 Matches 57; Conservative 29; Mismatches 39; Indels 3; Gaps 2;

OY 1 DIECPGSGSSTDRYCYKPFKQEMTWASARFCSEQAKGHLISVETALASFDVNLVYANKE 60  
 DB 1 DRCPTWASASLYCYKPFKQEMTWASARFCSEQAKGHLISVETALASFDVNLVYANKE 60  
 OY 61 KEYLRYIWMIGLRVNGKQPCSSSYENLVDPFE--ECFMWSRDRTRLEMPKVDK 117  
 DB 61 FDKQRYRATVGLTERNLKMTNGASVYENWIEASKECTGLGKETGFRKWNVYCG 120  
 OY 118 FICKETFP 125  
 DB 121 FICKETFP 128

RESULT 15  
 ID ABBA TRIAB STANDARD; PRT; 132 AA.  
 AC P8115;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Albogreggin B alpha subunit.  
 OS Trimeresurus albolabris (White-lipped pit viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 OX NCBI\_Taxid=8765;  
 CC -1- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.  
 CC -1- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=15184.53; MW\_ERR=2.74; METHOD=Electrospray;  
 CC RANGE=1-129; NOTE=Ref.1.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 DR HSSP; P22030; I10K.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00611; C\_TYPE\_LLECTIN\_2; 1.  
 KW Direct protein sequencing; Lectin.  
 FT DOMAIN 3 125 C-type lectin.  
 FT DISULFID 4 15 By similarity.  
 FT DISULFID 98 115 By similarity.  
 SQ SEQUENCE 129 AA; 15190 MW; EFAB318FAC8070AE CRC64;



RA Calvete J.J., Niewiarowski S.;  
 RT "Alboaggregine A and B. Structure and interaction with human platelets";  
 RL Thromb. Haemost. 79:609-613(1998).  
 CC -1- FUNCTION: Binds to platelet GPIIb/IX receptor system and stimulates aggregation.  
 CC -1- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 DR HSSP; P23806; 1J34.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Direct protein sequencing; Lectin.  
 FT DOMAIN 1 132  
 FT DISULFID 2 13  
 FT DISULFID 30 127  
 FT DISULFID 79 79  
 FT By similarity.  
 FT Interchain (with C-75 in beta chain) (By similarity).  
 FT DISULFID 102 119  
 FT By similarity.  
 SQ SEQUENCE 132 AA; 15419 MW; 6FA864820383F16F CRC64;

Query Match 45.3%; Score 314.5; DB 1; Length 132;  
 Best Local Similarity 46.5%; Pred. No. 2.7e-25;  
 Matches 60; Conservative 20; Mismatches 40; Indels 9; Gaps 2;

QY 3 ECPSGMSSTRDYCYKPFKQEMTWASAEFSCSQAKGHLISVETALBASVFNVLVYANKE 62  
 DB 1 DCPSPMSSEKQYCYQVIVKELKWEDEKXFCSEQANDGHVLSISYEAVFVALLSENYX 60  
 QY 63 YLTRYWIYIGLRVQNGQPC-----SSISYENLVDP--ECFVNSDTRLREMFVXD 113  
 DB 61 XXXYHWIGLSVGNKQKQCSSEMSDSSVYENLVIXXXKCFVLKKESEFRITWSNVYCH 120  
 QY 114 QQHSFICKF 122  
 DB 121 QKHIFCKF 129

RESULT 16  
 Q8AYAS PRELIMINARY; PRT; 158 AA.  
 AC 08AYAS;  
 DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-OCT-2003 (TEMBLrel. 23, Last sequence update)  
 DE Agglucetin-alpha 2 subunit precursor.  
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Deinagkistrodon.  
 OC NCBI\_TaxID=36307;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21542539; PubMed=11686327;  
 RA Wang W.-J., Huang T.-F.;  
 RT "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein IB agonist";  
 RL Thromb. Haemost. 86:1077-1086(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22839357; PubMed=12958616;  
 RA Wang W.-J., Ling Q.-D., Liu M.-Y., Huang T.-F.;  
 RT "A tetrameric glycoprotein IB-binding protein, agglucetin, from Formosan pit viper: structure and interaction with human platelets";  
 RL Thromb. Haemost. 90:465-475(2003).  
 DR EMBL; AF540646; AAN23125.1; -.  
 DR HSSP; P23806; 1J34.  
 DR GO; GO:0005529; F:sugar binding; IBA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatis\_ac.

DR Pfam; PF00059; Lectin\_C; 1.  
 DR PRINTS; PRO1504; PNCREATTSP.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 158  
 FT agglucetin-alpha 2 subunit.  
 SQ SEQUENCE 158 AA; 17977 MW; 9D0A9C36ABEA5E4 CRC64;

Query Match 45.3%; Score 314.5; DB 2; Length 158;  
 Best Local Similarity 43.5%; Pred. No. 3.2e-25;  
 Matches 57; Conservative 25; Mismatches 40; Indels 9; Gaps 2;

QY 1 DLECPGMSSTRDYCYKPFKQEMTWASAEFSCSQAKGHLISVETALBASVFNVLVYAN 60  
 DB 24 DENCPRGMSAYQCYQVIVKERNMDARFCTEQADGSHVLSIEKGRDPVLAQVSN 83  
 QY 61 KEYLTRYWIYIGLRVQNGQPC-----SSISYENLVDP--ECFVNSDTRLREMFVXD 111  
 DB 84 ISVEDHWVTGLRVQNGKQCSSTWEDGSSVSEYENLVKRCGALERTGFHKWING 143  
 QY 112 CEQHSFICKF 122  
 DB 144 CQLNPFCKF 154

RESULT 17  
 BOTA\_BOTJA STANDARD; PRT; 133 AA.  
 AC BOTA\_BOTJA;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Botrocetin, alpha chain (platelet coagglutinin).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE=Venom;  
 RX MEDLINE=93157385; PubMed=8430107;  
 RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H., Titani K.;  
 RT "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).  
 RN [2]  
 RP SEQUENCE OF 1-40.  
 RC TISSUE=Venom;  
 RX MEDLINE=91129280; PubMed=1993206;  
 RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;  
 RT "Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca";  
 RL Biochemistry 30:1957-1964(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=22118144; PubMed=12121649; DOI=10.1016/S0969-2126(02)00787-6;  
 RA Fukuda K., Doggett T.A., Bankston U.A., Cruz M.A., Diacovo T.G., Liddington R.C.;  
 RT "Structural basis of von Willebrand factor activation by the snake toxin botrocetin";  
 RL Structure 10:943-950(2002).  
 CC -1- FUNCTION: Two-chain botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPIb, resulting in platelet aggregation.  
 CC -1- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain botrocetin in promoting vWF

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CC      binding to platelets.
CC      -1- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC      Botrocelin and wvr form a soluble complex.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR      PIR: A47267; A47267.
DR      PDB: 1FVU; X-ray; A/C=1-133.
DR      PDB: 1LJK; X-ray; B=1-133.
DR      InterPro: IPR002353; AntiFreezeII.
DR      InterPro: IPR01304; Lectin_C.
DR      Pfam: PF00059; Lectin_C.
DR      PRINTS: PR00356; ANTIFREEZEII.
DR      SMART: SM00034; CLECT_1.
DR      PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR      PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW      3d-structure; Direct protein sequencing; Lectin.
FT      DISULFID 30 128
FT      DISULFID 80 80
FT      DISULFID 103 120
FT      TURND 4 5
FT      STRAND 7 9
FT      TURND 10 11
FT      STRAND 12 21
FT      HELIX 22 33
FT      TURND 35 36
FT      STRAND 38 39
FT      TURND 44 45
FT      TURND 47 47
FT      HELIX 48 57
FT      TURND 58 59
FT      TURND 62 63
FT      STRAND 66 73
FT      STRAND 83 83
FT      STRAND 85 86
FT      STRAND 89 89
FT      STRAND 95 95
FT      HELIX 97 99
FT      STRAND 103 107
FT      TURND 108 111
FT      STRAND 115 118
FT      TURND 120 121
FT      STRAND 124 130
SQ      SEQUENCE 133 AA; 15215 MW; E4CF4502946ACT74B CRC64;

Query Match      44.7%; Score 311; DB 1; Length 133;
Best Local Similarity 45.9%; Pred. No. 6.3e-25;
Matches 61; Conservative 24; Mismatches 38; Indels 10; Gaps 3;

QY      3 ECPGSGMSSTDYCYKPKQEMTWASAEKFCSEQAKGHLISVET-ALASFDVNLVYANK 61
DB      1 DCPGSGMSYEGNCKYKFKFOQKMNWADAEKFCSEQAKGHLISVETSKEDPFVDLVTXNI 60
QY      62 EYLTIRIWIIGLRVONKGPC-----SSISYENLVDPF--ECFVWSRDTLRLEWFKVDC 112
DB      61 QSSDLVYIIGLRVENEKQCSSEWSSGSSVYENVETVKCFALFKDLGFVLMINLVC 120

QY      113 EQQHSFICKFTRP 125
DB      121 AQKPFVCKSPPP 133

RESULT 18
Q8AV97      PRELIMINARY; PRT; 158 AA.
AC      08AV97;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Flavocetin-A alpha chain.
OS      Trimeresurus flavoviridis (Habu) (Procyonidae: Trimeresuridae: Eucalloscomi:
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

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OC      viperidae; Crocotalinae; Trimeresurus.
ON      NCBI_TaxID=88087;
RX      11)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Venom glands;
RX      MEDLINE=20402624; PubMed=10942790; DOI=10.1016/S0049-3848(00)00234-6;
RA      Shin Y., Okuyama I., Hasegawa J., Morita T.;
RT      "Molecular cloning of glycoprotein Ib-binding protein, flavocetin-A,
RT      which inhibits platelet aggregation."
RL      Thromb. Res. 99:239-247(2000).
RN      12)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Venom glands;
RA      Shin Y., Okuyama I., Hasegawa J., Morita T.;
RL      Submitted (SEP-2002) to the EMBL/GenBank/DBD databases.
DR      EMBL: AY149341; AN172438.1; -.
DR      PDB: 1CJA; X-ray; A=24-157.
DR      GO: GO:0005529; F.sugar binding; IEA.
DR      InterPro: IPR001304; Lectin_C.
DR      InterPro: IPR003990; Pancrreatis_ac.
DR      Pfam: PF00059; Lectin_C; 1.
DR      PRINTS: PR01504; PNCREATITISAP.
DR      SMART: SM00034; CLECT_1.
DR      PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR      PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
SQ      SEQUENCE 158 AA; 18073 MW; 8C138650665CA454 CRC64;

Query Match      44.7%; Score 310.5; DB 2; Length 158;
Best Local Similarity 42.4%; Pred. No. 8.6e-25;
Matches 56; Conservative 24; Mismatches 43; Indels 9; Gaps 2;

QY      1 DLECPGMSSTDYCYKPKQEMTWASAEKFCSEQAKGHLISVETALASFDVNLVYANK 60
DB      24 DPCDIPGWSAYDRYCYQAFSKPKNWDASFCBEQKSHLVSISSGSDVVAOLVARK 83
QY      61 KEYLIRIWIIGLRVONKGPC-----SSISYENLVDPF--ECFVWSRDTLRLEWFKVDC 111
DB      84 IKTSFQYWIIGLRVONKQCSSEWSSGSSVYENVETVKCFALFKDLGFVLMINLVC 143

QY      112 EQQHSFICKFTRP 123
DB      144 CGTENPFVCKYT 155

RESULT 19
Q8UVVC6      PRELIMINARY; PRT; 158 AA.
AC      08UVVC6;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Antithrombin 1 A chain.
OS      Agkistrodon acutus (hundred-pace snake) (Dinagkistrodon acutus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Viperidae; Crocotalinae; Deinagkistrodon.
ON      NCBI_TaxID=36307;
RX      11)
RP      SEQUENCE FROM N.A.
RA      Yu H., Xiang K., Liu J.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBD databases.
DR      EMBL: AF463522; AF463522.1; -.
DR      HSSP: P23806; 1J34.
DR      GO: GO:0005529; F.sugar binding; IEA.
DR      Pfam: PF00059; Lectin_C; 1.
DR      PRINTS: PR01504; PNCREATITISAP.
DR      SMART: SM00034; CLECT_1.
DR      PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR      PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
SQ      SEQUENCE 158 AA; 17950 MW; A73A9C895997BFD7 CRC64;

Query Match      44.5%; Score 309.5; DB 2; Length 158;
Best Local Similarity 42.7%; Pred. No. 1.1e-24;

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RX MEDLINE=22839357; PubMed=12958616;  
 RA Wang W.-J., Ling Q.-D., Liao M.-Y., Huang T.-F.;  
 RT "A tetrameric glycoprotein Ib-binding protein, agglutecetin, from  
 RT Thrombospondin type 1 domain protein 1 (TSP1) interacts with human platelets";  
 RL Thromb. Haemost. 90:465-475(2003).  
 DR EMBL: AY091759; AAC22787.1; -.  
 DR EMBL: AF540645; AAC23124.1; -.  
 DR HSSP: P23806; 1J34.  
 DR GO: GO:0005529; F:sugar binding; IEA.  
 DR InterPro: IPR001304; Lectin\_C.  
 DR InterPro: IPR003990; Pancreatis\_ac.  
 DR Pfam: PF00059; Lectin\_C; 1.  
 DR PRINTS: PR01504; PNCREATITSAF.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Lectin; signal.  
 FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 154 agglutecetin-alpha 1 subunit.  
 SQ SEQUENCE 154 AA; 17317 MW; AA08E518501BECC7 CRC64;

Query Match 43.8%; Score 304.5; DB 2; Length 154;  
 Best Local Similarity 41.5%; Pred. No. 3.6e-24;  
 Matches 54; Conservative 32; Mismatches 33; Indels 11; Gaps 3;

QY 1 DECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFYDNLVYAN 60  
 DB 24 DVDCLFGMSAVDQSCYRFFLTKTMDAEKFTERRPKGHLVIESAGRDFVAQJVSNN 83  
 QY 61 KEVLTFTYITIGLRVONKQGPC-----SSISENVLVD--PFCFVNSDTRLRKFKVD 111  
 DB 84 KQ--TNNVWLGILGKIQSGQOCSTEWTDGSSVSSEYKSKCFYLEKNTGRTWLINLN 141  
 QY 112 CEQHSFICK 121  
 DB 142 CGSEYAFVCK 151

RESULT 23  
 QYGN5 PRELIMINARY; PRT; 154 AA.  
 AC QYGN5;  
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Fibrinogen clotting inhibitor A chain.  
 OS Agkistrodon halys brevicaudus (Korean slanders snake) (Gloydinus halys brevicaudus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;  
 OC Viperidae; Crotalinae; Gloydus.  
 OX NCBI\_TaxID=259325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kim D.S., Koh Y.S.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF125309; AAD18055.1; -.  
 DR HSSP: P23806; 1J34.  
 DR GO: GO:0005529; F:sugar binding; IEA.  
 DR InterPro: IPR001304; Lectin\_C.  
 DR InterPro: IPR003990; Pancreatis\_ac.  
 DR Pfam: PF00059; Lectin\_C; 1.  
 DR PRINTS: PR01504; PNCREATITSAF.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 154 AA; 17293 MW; 8D06F7DDFA0D140D CRC64;

Query Match 43.8%; Score 304.5; DB 2; Length 154;  
 Best Local Similarity 44.6%; Pred. No. 3.6e-24;  
 Matches 58; Conservative 20; Mismatches 43; Indels 9; Gaps 2;

QY 1 DECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFYDNLVYAN 60

DB 24 DECPGMSNNHGCHQAFNQMRTWEDAEFCSQAKGHLISVETALASFYDNLVYAN 83  
 QY 61 KEVLTFTYITIGLRVONKQGPC-----SSISENVLVDPF--CFVNSDTRLRKFKVD 111  
 DB 84 IETSPPHWITIGLRDEKQCCSSMSDSSVSSEYKSKCFYLEKNTGRTWLINLN 143  
 QY 112 CEQHSFICK 121  
 DB 144 CGRNPFVCE 153

RESULT 24  
 QYGN5 PRELIMINARY; PRT; 146 AA.  
 AC QYGN5;  
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Factor XI/Factor X binding protein A chain.  
 GN Name=XI/Xbp-a;  
 OS Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 OX NCBI\_TaxID=88087;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshinaru M., Chijiwa T.,  
 RA Chang C., Fukumaki Y., Ono M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB046491; BAB21452.1; -.  
 DR HSSP: P23806; 1IXX.  
 DR GO: GO:0005529; F:sugar binding; IEA.  
 DR InterPro: IPR001304; Lectin\_C.  
 DR InterPro: IPR003990; Pancreatis\_ac.  
 DR Pfam: PF00059; Lectin\_C; 1.  
 DR PRINTS: PR01504; PNCREATITSAF.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 146 AA; 16461 MW; 6ADP0E032544316C CRC64;

Query Match 43.5%; Score 302.5; DB 2; Length 146;  
 Best Local Similarity 44.5%; Pred. No. 5.5e-24;  
 Matches 57; Conservative 25; Mismatches 37; Indels 9; Gaps 2;

QY 3 ECPGMSSTDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALASFYDNLVYANKE 62  
 DB 18 DCLSGMSYEGHCYAFKFKYKTEWEDAEKFTERRPKGHLVIESAGRDFVAQJVSNN 77  
 QY 63 YLTFTYITIGLRVONKQGPC-----SSISENVLVDPF--CFVNSDTRLRKFKVD 113  
 DB 78 RLDFYITIGLRVONKQKQNSMSDSSVSSEYKSKCFYLEKNTGRTWLINLN 137  
 QY 114 QCHSFICK 121  
 DB 138 QGNPFVCE 145

RESULT 25  
 IXA TRIPL STANDARD; PRT; 152 AA.  
 AC P23806; Q91246;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Coagulation factor IX/factor X-binding protein A chain precursor  
 DE (IX/X-BP).  
 OS Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;

OC Viperidae; Crocodylia; Trimeresurus.  
 OX NCBI\_TaxID=88087;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96184662; PubMed=8645314; DOI=10.1006/bbrc.1996.0414;  
 RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;  
 RT "cDNA Cloning of IX-X-BP, a heterogeneous two-chain anticoagulant  
 protein from snake venom.";  
 RL Biochem. Biophys. Res. Commun. 220:382-387 (1996).  
 RN [2]  
 RP SEQUENCE OF 24-152.  
 RC TISSUE=Venom;  
 RX MEDLINE=91332000; PubMed=1831197;  
 RA Atoda H., Hyuga M., Morita T.;  
 RT "The primary structure of coagulation factor IX/factor X-binding  
 protein isolated from the venom of Trimeresurus flavoviridis. Homology  
 with asialoglycoprotein receptors, proteoglycan core protein,  
 tetraectin, and lymphocyte Fc epsilon receptor for immunoglobulin  
 E.";  
 RL J. Biol. Chem. 266:14903-14911 (1991).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC TISSUE=Venom;  
 RX PubMed=874314;  
 RA Atoda H., Ishikawa M., Yoshihara E., Sekiya F., Morita T.;  
 RT "Blood coagulation factor IX-binding protein from the venom of  
 Trimeresurus flavoviridis: purification and characterization.";  
 RL J. Biochem. 118:965-973 (1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=97331317; PubMed=9187649;  
 RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;  
 RT "Structure of coagulation factors IX/X-binding protein, a heterodimer  
 of C-type lectin domains.";  
 RL Nat. Struct. Biol. 4:438-441 (1997).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).  
 RX PubMed=10339409; DOI=10.1006/jmbi.1999.2756;  
 RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;  
 RT "Crystal structure of coagulation factor IX-binding protein from habu  
 snake venom at 2.6 A: implication of central loop swapping based on  
 deletion in the linker region.";  
 RL J. Mol. Biol. 289:103-112 (1999).  
 CC -1- FUNCTION: Anticoagulant protein which binds with factor IX and  
 factor X in the presence of calcium with a 1 to 1 stoichiometry.  
 CC -1- SUBUNIT: Heterodimer of chains A and B, disulfide-linked.  
 CC -1- MISCELLANEOUS: Calcium is required for ligand binding.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D83331; BAA11887.1; -;  
 DR PIR; JCA690; JCA690.  
 DR PDB; 1IXX; X-ray; A/C/E=24-152.  
 DR PDB; 1UJ4; X-ray; A=24-152.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatic\_ac.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR PRINTS; PRO1504; PNCREATITAP.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_2; 1.  
 DR 3D-structure; Calcium; Direct protein sequencing; Lactin; Signal.  
 KW SIGNSL 1 23  
 FT CHAIN 24 152  
 FT Coagulation factor IX/factor X-binding  
 FT protein A chain.

FT DOMAIN 24 152 C-type lectin.  
 FT DISULFID 25 36  
 FT DISULFID 53 150  
 FT DISULFID 102 102 Interchain (with C-98 in chain B).  
 FT DISULFID 125 142  
 FT TURN 27 28  
 FT STRAND 30 32  
 FT TURN 33 34  
 FT STRAND 35 44  
 FT STRAND 35 44  
 FT HELIX 46 54  
 FT TURN 55 56  
 FT TURN 58 59  
 FT STRAND 61 62  
 FT HELIX 68 81  
 FT STRAND 89 95  
 FT STRAND 105 105  
 FT TURN 107 108  
 FT STRAND 111 111  
 FT STRAND 117 117  
 FT HELIX 119 121  
 FT STRAND 125 128  
 FT HELIX 130 132  
 FT TURN 133 134  
 FT STRAND 137 140  
 FT TURN 142 143  
 FT STRAND 146 152  
 SQ SEQUENCE 152 AA; 17213 MW; FB3DD236900263 CRC64;  
 Query Match 43.5%; Score 302.5; DB 1; Length 152;  
 Best Local Similarity 44.5%; Pred. No. 5, 8e-24;  
 Matches 57; Conservative 25; Mismatches 37; Indels 9; Gaps 2;  
 QY 3 ECPSSGWSYDRCYKPEKQEMTMSAERFCSQAKGHLSTVETALASPVNDLVANKE 62  
 Db 24 DCLSGWSYEGHCYKPEKKTWEDAEKVCITDQAKAHVSISSGEADPVAQVLQNK 83  
 QY 63 YLTREYTWIGLRYQNKQPC-----SSISYENVDPFE--CEWVSRRDLREMFVDCB 113  
 Db 84 RLDFYTWIGLRYQNKQKQNSEMSDSSVSYENWIEASKTCGLEKETDFRMVNIYCG 143  
 QY 114 QQHSFICK 121  
 Db 144 QQNPFCVE 151  
 RESULT 26  
 ID 08UGT7 PRELIMINARY; PRT; 158 AA.  
 AC 08UGT7;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE C-type lectin-like protein TMVA A chain.  
 OS Trimeresurus mucrosquamatus (Taiwan habu) (Protothrops  
 OS mucrosquamatus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosteura; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crocodylia; Protothrops.  
 OX NCBI\_TaxID=103944;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22210230; PubMed=12220719; DOI=10.1016/S0041-0101(02)00144-7;  
 RA Wei Q., Lu Q.M., Jin Y., Li R., Wei J.F., Wang W.Y., Xiong Y.L.;  
 RT "Purification and cloning of a novel C-type lectin-like protein with  
 platelet aggregation activity from Trimeresurus mucrosquamatus  
 venom.";  
 RL Toxicol. 40:1331-1338 (2002).  
 DR EMBL; AY099321; AAM43808.1; -;  
 DR PDB; 1V4L; X-ray; A/C/E=24-158.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatic\_ac.  
 DR Pfam; PF00059; Lectin\_C; 1.

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DR PRINTS, PRO1504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00615; C TYPE LECTIN 2; 1.
DR LECTIN.
SQ SEQUENCE 158 AA; 18101 MW; CD087102289AA6E CRC64;

Query Match 43.2%; Score 300.5; DB 2; Length 158;
Best Local Similarity 40.9%; Pred. No. 9.9e-24;
Matches 54; Conservative 25; Mismatches 44; Indels 9; Gaps 2;

QY 1 DLECPGSGSTDRYCYKPFKQENTMASARFCSEQAKGHLISVETALASFPDNLVLYAN 60
DB 24 DFDCLPGWSAYDRYCYQAFSEPKNWDASFCEGVKTSHTLVSISSGGDFVAQLVAEK 83
QY 61 KEVLTFTYVIGLTVQKQGPC-----SISYENIV--DPECFWVSRTLRLEWFKVD 111
DB 84 IKTSPFYVWIGLRIQKKEQCRSEMSDASVYENILFKSSKKCYALKKGTETLRFTFNVY 143
QY 112 CEQOHSFICKFT 123
DB 144 CGRENPFVCKYT 155

RESULT 27
Q6TPHO PRELIMINARY; PRT; 158 AA.
AC 06TPHO;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Mucrocelin alpha chain.
OS Trimeric mucusquamous (Taiwan habu) (Protobothrops
OC mucusquamous).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Protobothrops.
OX NCBI_TaxID=103944;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Hung C.-C., Huang K.-F., Chlou S.-H.;
RL Submitted (Sep-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY390533; AAQ93686.1; -.
DR GO; GO:000529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; LECTIN_C; 1.
DR PRINTS; PRO1504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00615; C TYPE LECTIN 2; 1.
SQ SEQUENCE 158 AA; 18125 MW; 419ABE2F0344B9CA CRC64;

Query Match 43.2%; Score 300.5; DB 2; Length 158;
Best Local Similarity 40.9%; Pred. No. 9.9e-24;
Matches 54; Conservative 25; Mismatches 44; Indels 9; Gaps 2;

QY 1 DLECPGSGSTDRYCYKPFKQENTMASARFCSEQAKGHLISVETALASFPDNLVLYAN 60
DB 24 DFDCLPGWSAYDRYCYQAFSEPKNWDASFCEGVKTSHTLVSISSGGDFVAQLVAEK 83
QY 61 KEVLTFTYVIGLTVQKQGPC-----SISYENIV--DPECFWVSRTLRLEWFKVD 111
DB 84 IKTSPFYVWIGLRIQKKEQCRSEMSDASVYENILFKSSKKCYALKKGTETLRFTFNVY 143
QY 112 CEQOHSFICKFT 123
DB 144 CGRENPFVCKYT 155

RESULT 28
CVXA_CRODU

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ID CVXA_CRODU STANDARD; PRT; 158 AA.
AC 093426;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Convulxin alpha precursor (CVX alpha).
OS Crocacin durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-46; 61-68; 108-120; 139-145 AND
RP 149-153.
RC TISSUE=Venom gland;
RX MEDLINE=98324901; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
RT aggregating protein from Crotalus durissus terrificus venom.",
RT Biochem. J. 333:389-393(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 24-158.
RX PubMed=14521935; DOI=10.1016/j.jbc.2003.09.032;
RA Murakami M.T., Zela S.P., Gava L.M., Michelen-Duarte S.,
RA Cintra A.C.O., Arni R.K.;
RT "Crystal structure of the platelet activator convulxin, a disulfide-
RT linked alpha4beta4 cyclic tetramer from the venom of Crotalus durissus
RT terrificus.",
RT Biochem. Biophys. Res. Commun. 310:478-482(2003).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 26-158.
RX PubMed=14684891;
RA Batuwangala T., Leduc M., Gibbins J.M., Bon C., Jones E.Y.;
RT "Structure of the snake-venom toxin convulxin.",
RL Acta Crystallogr. D 60:46-53(2004).
CC -1- FUNCTION: Binds to the platelet and collagen receptor,
CC glycoprotein VI (GPVI).
CC -1- SUBUNIT: Heterodimer of four alpha chains and four beta chains;
CC disulfide-linked.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Y16348; CAA76181.1; -.
DR EMBL; AF541882; AAQ11363.1; -.
DR PDB; 1UWR; X-ray; A/B=24-157.
DR PDB; 1UWR; X-ray; A/C=24-157.
DR InterPro; IPR001304; LECTIN_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; LECTIN_C; 1.
DR PRINTS; PRO1504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00615; C TYPE LECTIN 2; 1.
KW 3D-structure, Direct protein sequencing, Glycoprotein, Lectin, Signal.
FT SIGNAL 1 23
FT CHAIN 24 158 Convulxin alpha.
FT DOMAIN 34 158 C-type lectin.
FT DISULFID 27 38
FT DISULFID 55 152
FT DISULFID 104 104 Interchain (with C-100 in beta chain).
FT DISULFID 127 144

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FT DISULFID 158 158 Interchain (with C-26 in beta chain).
SQ SEQUENCE 158 AA; 18141 MW; 949F9C6D673E2318 CRC64;

Query Match
Best Local Similarity 43.1%; Score 293.5; DB 1; Length 158;
Matches 56; Conservative 27; Mismatches 38; Indels 9; Gaps 2;

QY 2 LECPSGMSSTRDYCYKPFKQEMTWASAEFCSOAKGCHLLSVETALBASFDVNLVYANK 61
DB 25 LHCPSDMYYVDQHCYRIFNEENMMDAEWECTKQAKGHLVSIKSAKEADFAVMYTONI 84
QY 62 EVLTRYIMIGLRVONKQGPC-----SSISYENLVDPF--ECPMVSRLRLREMPKVDG 112
DB 85 EESFSFVSIGLRVONKQKOCSTKSDGSSVSDNLDLVYTKSLKKEGTGRKMFVASC 144
QY 113 EOHSPICKP 122
DB 145 ICKIPFVCKP 154

RESULT 29
Q9DG39 PRELIMINARY; PRT; 152 AA.
AC Q9DG39;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Halysin A-chain precursor.
GN Name=HXNA;
OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydine halys
OS pallasi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OC NCB1_Taxid=8714;
RN (1)
RP SEQUENCE FROM N.A.
RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF190827; AAC17178.1; -.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lactin_C.
DR InterPro; IPR003990; Pancreat_ ac.
DR Pfam; PF00059; Lactin_C; 1.
DR PRINTS; PR01504; PNCREATITTSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LACTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LACTIN_2; 1.
KW Signal.
FT CHAIN 1 23 Potential.
FT SIGNAL 24 152 halysin A-chain.
SQ SEQUENCE 152 AA; 17455 MW; BDD7AD1DC280C28D CRC64;

Query Match
Best Local Similarity 41.4%; Score 292.5; DB 2; Length 152;
Matches 53; Conservative 27; Mismatches 39; Indels 9; Gaps 2;

QY 3 ECPGMSSTRDYCYKPFKQEMTWASAEFCSOAKGCHLLSVETALBASFDVNLVYANK 62
DB 24 DCPGMSSTRDYCYKPFKQEMTWASAEFCSOAKGCHLLSVETALBASFDVNLVYANK 83
QY 63 YLTRYIMIGLRVONKQGPC-----SSISYENLVDPF--ECPMVSRLRLREMPKVDG 113
DB 84 RGIYIMIGLRVONKQKQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSS 143
QY 114 OQHSPICK 121
DB 144 ERNPFVCE 151

RESULT 30
Q8J1W0

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ID O8J1W0 PRELIMINARY; PRT; 152 AA.
AC O8J1W0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ACF 1/2 A-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OC NCB1_Taxid=36307;
RN (1)
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091758; AAM22786.1; -.
DR PIR; JC7134; JC7134.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lactin_C.
DR InterPro; IPR003990; Pancreat_ ac.
DR Pfam; PF00059; Lactin_C; 1.
DR PRINTS; PR01504; PNCREATITTSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LACTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LACTIN_2; 1.
SQ SEQUENCE 152 AA; 17108 MW; B0870F3DA0A4D23B CRC64;

Query Match
Best Local Similarity 41.5%; Score 288.5; DB 2; Length 152;
Matches 55; Conservative 24; Mismatches 40; Indels 9; Gaps 2;

QY 3 ECPGMSSTRDYCYKPFKQEMTWASAEFCSOAKGCHLLSVETALBASFDVNLVYANK 62
DB 24 DCPGMSSTRDYCYKPFKQEMTWASAEFCSOAKGCHLLSVETALBASFDVNLVYANK 83
QY 63 YLTRYIMIGLRVONKQGPC-----SSISYENLV--DPFECMVSRLRLREMPKVDG 113
DB 84 SAKIHWIGLRVONKQKQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSSQSS 143
QY 114 OQHSPICK 121
DB 144 QRPDFVCE 151

RESULT 31
Q9DEF9 PRELIMINARY; PRT; 152 AA.
AC Q9DEF9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anticoagulant protein A precursor.
GN Name=acp-a;
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OC NCB1_Taxid=36307;
RN (1)
RP SEQUENCE FROM N.A.
RA Tissue=Venom gland;
RL MEDLINE=22167433; PubMed=12175618; DOI=10.1016/S0041-0101(01)00289-6;
RA Tani A., Ogawa T., Nose T., Nikandrov N.N., Deshimaru M., Chijiwa T.,
RA Chang C.C., Fukumaki Y., Ohno M.;
RT "Characterization, primary structure and molecular evolution of
RT anticoagulant protein from Agkistrodon acutus venom.";
RL Toxicon 40:803-813 (2002)
DR EMBL; AB036880; BAA99281.1; -.
DR PIR; JC7134; JC7134.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lactin_C.

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DR InterPro; IPR003990; Pancreatis\_ac.  
 DR Pfam; PF00059; Lectin\_C.1.  
 DR PRINTS; PR01504; PNCREATITISAP.  
 DR SMART; SM00034; CLECT.1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00641; C\_TYPE\_LLECTIN\_2; 1.  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 152 AA; 17124 MW; 5C59C0F503A4D223 CRC64;

Query Match 41.4%; Score 288.5; DB 2; Length 152;  
 Best Local Similarity 43.0%; Pred. No. 1.8e-22;  
 Matches 55; Conservative 24; Mismatches 40; Indels 9; Gaps 2;

QY 3 ECPGSGSTDRYCYKPFKQEMTWASAEFCSQAQKGHLSVETALASFDVNLANK 62  
 DB 24 DCSGSSSYEGHYKFKOSKTMADAESECTKQVNGHLSVSSGEADPVALIQAOKIK 83  
 QY 63 YLTRVYIGLRVONKQOPC-----SSISYENLV--DPFECFMSRDTRLREMFVDC 113  
 DB 84 SAKIHWIGLRQNKKEKQCSSEMSDSSISYENWIEESKCLGVHAKTGFRKMFVCE 143  
 QY 114 QQHSFICK 121  
 DB 144 QDDPFVCE 151

## RESULT 32

Q91841 PRELIMINARY; PRT; 136 AA.

ID Q91841  
 AC Q91841  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Aggretin alpha chain (Fragment).  
 OS Agkistrodon rhodostoma (Malayan pit viper) (Collolelasma rhodostoma).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Calloselasma.  
 NX NCBI\_TaxID=8717;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RX MEDLINE=99443731; PubMed=10512747; DOI=10.1006/dbrc.1999.1457;  
 RA Chung C.H., Au L.C., Huang T.F.;  
 RT "Molecular cloning and sequence analysis of aggretin, a collagen-like  
 RT platelet aggregation inducer";  
 RT Biochem. Biophys. Res. Commun. 263:723-727(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RA Chung C.H., Au L.C., Huang T.F.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP244900; AAF79952.1; -.  
 DR PIR; PC7027; PC7027.  
 DR HSP; P23806; J34.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatis\_ac.  
 DR Pfam; PF00059; Lectin\_C.1.  
 DR PRINTS; PR01504; PNCREATITISAP.  
 DR SMART; SM00034; CLECT.1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00641; C\_TYPE\_LLECTIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 136  
 SQ SEQUENCE 136 AA; 15796 MW; 3B474A4149F0027A CRC64;

Query Match 41.4%; Score 288; DB 2; Length 136;  
 Best Local Similarity 43.8%; Pred. No. 1.8e-22;  
 Matches 57; Conservative 21; Mismatches 40; Indels 12; Gaps 4;

QY 3 ECPGSGSTDRYCYKPFKQEMTWASAEFCSQAQKGHLSVETALASFDVNLANK 62

DB 4 DDDFMSPYDCHCYAFNEQKWDAAEKFCRAQENGALHASTESNGEDFV-SWITSQKD 62  
 QY 63 YLT--RYIWIGLRVONKQOPC-----SSISYENLV--DPFECFMSRDTRLREMFVDC 111  
 DB 63 ELADEDYVWIGLRQNKKEKQCSSEMSDSSISYENWIEESKCLGVHAKTGFRKMFVCE 122  
 QY 112 CEQHSFICK 121  
 DB 123 CEQMAFVCK 132

## RESULT 33

Q91AM1 PRELIMINARY; PRT; 152 AA.

ID Q91AM1  
 AC Q91AM1  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).  
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Deinagkistrodon.  
 NX NCBI\_TaxID=36307;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom;  
 RA Yu H.-X., Xiang K.-J., Liu J.;  
 RT "cDNA sequencing and analysis of eleven C-type lectin-like protein  
 RT subunits from Agkistrodon acutus";  
 RT Acta Biochim. Biophys. Sin. 0:0-0(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom;  
 RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,  
 RA Liu J.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom;  
 RA Yu H.-X., Xiang K.-J., Wang Y., Liu J.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP176420; AAF26286.2; -.  
 DR PIR; JC7134; JC7134.  
 DR HSP; P23806; J34.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatis\_ac.  
 DR Pfam; PF00059; Lectin\_C.1.  
 DR PRINTS; PR01504; PNCREATITISAP.  
 DR SMART; SM00034; CLECT.1.  
 DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE; PS00641; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 152 AA; 17109 MW; 76A0F636DBF0D7AB CRC64;

Query Match 41.4%; Score 287.5; DB 2; Length 152;  
 Best Local Similarity 43.0%; Pred. No. 2.2e-22;  
 Matches 55; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 3 ECPGSGSTDRYCYKPFKQEMTWASAEFCSQAQKGHLSVETALASFDVNLANK 62  
 DB 24 DCSGSSSYEGHYKFKOSKTMADAESECTKQVNGHLSVSSGEADPVALIQAOKIK 83  
 QY 63 YLTRVYIGLRVONKQOPC-----SSISYENLV--DPFECFMSRDTRLREMFVDC 113  
 DB 84 SAKIHWIGLRQNKKEKQCSSEMSDSSISYENWIEESKCLGVHAKTGFRKMFVCE 143  
 QY 114 QQHSFICK 121  
 DB 144 QDDPFVCE 151



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RESULT 34
Q71RR4 ID 071RR4 PRELIMINARY; PRT; 152 AA.
AC 071RR4:
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Factor IX/X binding protein alpha chain.
OS Trimerus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Timereus.
OC NCB1_TaxID=39682;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Lee W.-H., Liu H., Zhang Y.,
RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354911; AA01513.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pncreatic_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00641; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 152 AA; 17092 MW; 2E355C3C01E243A CRC64;

Query Match 39.6%; Score 275.5; DB 2; Length 152;
Best Local Similarity 40.6%; Pred. No. 4.2e-21;
Matches 52; Conservative 25; Mismatches 42; Indels 9; Gaps 2;

QY 3 ECPGSGSSDTRYKPKFQKQMTASAEKRCSEQAKGHLISVETALASVVDNVLANK 62
DB 24 DCLSGSSSYEGHYKAFELYKTMEDAESEFCMEGKGLHVSISSEADPFAQLISENKK 83
QY 63 YLTRYTWIGLRVONKQGPC-----SSISYENLVDPFE--CFVSRDTRLREMFVDC 113
DB 84 RLDPFWWIGLRVQDEKQCNSEWSDSSVSYENWISSEKTKLGLQKQTKFRKRWNLVCG 143
QY 114 QOHSFICK 121
DB 144 QRIPFVCE 151

RESULT 35
Q696W1 ID 0696W1 PRELIMINARY; PRT; 158 AA.
AC 0696W1:
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Factor X activator light chain 2.
OS Vipera lebetina (Elephant snake) (Leventine viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Macrovipera.
OC NCB1_TaxID=8709;
[1]
RP SEQUENCE FROM N.A.
RA Sligur E., Aagpollu A., Trunmal K., Tonismaegi K., Tammlste I.,
RA Kalkinen N., Sligur J.,
RT "Factor X activator from Vipera lebetina venom is synthesized from
RT different genes."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY578116; AAT91068.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pncreatic_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITAP.
DR SMART; SM00034; CLECT; 1.

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DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00641; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 158 AA; 18093 MW; B1E628633627A015 CRC64;

Query Match 39.4%; Score 273.5; DB 2; Length 158;
Best Local Similarity 39.5%; Pred. No. 7.1e-21;
Matches 51; Conservative 27; Mismatches 42; Indels 9; Gaps 2;

QY 2 LCPGSGSSDTRYKPKFQKQMTASAEKRCSEQAKGHLISVETALASVVDNVLANK 61
DB 25 LDCPPDSSPYRYFCRVFKQKQMDAEKFCRRPNGLHVSISEEAEFVAQLISKIT 84
QY 62 EYLTRYTWIGLRVONKQGPC-----SSISYENLV--DPFECFVSRDTRLREMFVDC 112
DB 85 GKFTHTFWIGLRVQDEKQCNSEWSDSSVSYENWISSEKTKLGLQKQTKFRKRWNLV 144
QY 113 EQOHSFICK 121
DB 145 EEPYFVCK 153

RESULT 36
Q7SZVO ID 07SZVO PRELIMINARY; PRT; 121 AA.
AC 07SZVO:
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Factor IX binding protein A chain (Coagulation factor IX-binding
DE protein chain A) (Fragment).
OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydus halys
OS pallasi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OC NCB1_TaxID=8714;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Zang J., Teng M., Niu L.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY356354; AA016640.1; -.
DR EMBL; AY346127; AA024215.1; -.
DR HSSP; P23806; IJ34.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00641; C_TYPE_LLECTIN_2; 1.
FT NON TER 1
SQ SEQUENCE 121 AA; 13883 MW; FF7C84DD6A4B4765 CRC64;

Query Match 38.6%; Score 268.5; DB 2; Length 121;
Best Local Similarity 41.9%; Pred. No. 1.8e-20;
Matches 49; Conservative 25; Mismatches 34; Indels 9; Gaps 2;

QY 14 YCKPKQKQMTASAEKRCSEQAKGHLISVETALASVVDNVLANKYLTFTYTWIGLR 73
DB 4 HCYQTFKLRKRWADASFCTEQAKGHLVSDGADPFAQLVAENICKTETIYVWGLR 63
QY 74 VONKQGPC-----SSISYENLVDPFE--CFVSRDTRLREMFVDCQOHSFICK 121
DB 64 VQCKEQCCSEWSDSSVSYENWISSEKTKLGLQKQTKFRKRWNLVCG 120

RESULT 37
Q7T248 ID 07T248 PRELIMINARY; PRT; 131 AA.
AC 07T248:
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Schicetin A-chain.

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Query Match	37.7%;	Score 262;	DB 2;	Length 156;
Best Local Similarity	37.0%;	Pred. No. 1.2e-19;		

0y 1 DLEPCGMSSTDRCYKPFKXEMTWASERFCEQAKGHLSVETALEASFDVNVLYAN 6C

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Db 1 DODCLSGMSFYEGHCYOLFRLK-TWDEAKYCN-QMDGHLVSIENNAKAEFVAQLISRK 58
Qy 61 --KEYLTRIYIWIGLRVONKGPC-----SSISYENLVDPCECFWVSBDTRLREMFKYD 111
Db 59 LPKSAIEDRWVIGLDRSGKREOCQGHMTNOSFVHIVHPPTKCFVLEKOTERFKIAYVA 118
Qy 112 CEQOHSFICKFTRPR 126
Db 119 CEFKFPFVCKAKIPR 133

RESULT 40
08AYV4 PRELIMINARY; PRT; 146 AA.
AC 08AYV4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Agglucetin-beta 1 subunit precursor.
OS Agglucetodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OC NCB1_TaxID=36307;
RX MEDLINE=21542539; PubMed=11686327;
RA Wang W.-J., Huang T.-F.;
RT "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
RL Thromb. Haemost. 86:1077-1086(2001).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22839357; PubMed=12958616;
RA Wang W.-J., Ling Q.-D., Liu M.-Y.;
RT "A tetrameric glycoprotein ib-binding protein, agglucetin, from
RL Formosan pit viper: structure and interaction with human platelets.";
Thromb. Haemost. 90:465-475(2003).
DR EMBL; AF540647; XN23126.1; -.
DR HSRP; O93427; IUNR.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatic_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATTISAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Signal.
FT SIGNAL 1 23 potential.
FT CHAIN 24 146 agglucetin-beta 1 subunit.
SQ SEQUENCE 146 AA; 16728 MW; 2342BAE38E50CCB9 CRC64;

Query Match 36.8%; Score 255.5; DB 2; Length 146;
Best Local Similarity 43.2%; Pred. No. 5.3e-19;
Matches 54; Conservative 20; Mismatches 42; Indels 9; Gaps 5;

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AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Albogagregin A subunit 4. (white-lipped pit viper).
OS Trimeresurus albobabris (white-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OC NCB1_TaxID=8765;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Albogagregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -1- SUBUNIT: Heterotrimer of the subunits 1, 2, 3 and 4, disulfide-
CC linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSRP; P22030; IUNR.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Direct protein sequencing; Lectin.
FT DOMAIN 1 123 C-type lectin.
FT DISULFID 2 13 By similarity.
FT DISULFID 30 119 By similarity.
FT DISULFID 96 111 By similarity.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBEB1219C9B1E CRC64;

Query Match 36.3%; Score 252.5; DB 1; Length 123;
Best Local Similarity 39.7%; Pred. No. 9e-19;
Matches 52; Conservative 22; Mismatches 36; Indels 21; Gaps 6;

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Qy 3 ECPSGWSTDRYCYKPFKQEMTWASAEKRCSEQAKGHLISVETALBASFDVNYLANKR 62
Db 24 DCPSEWSSYEGHCYKAFKQSKTWADAEKFCQOHKSHLVSFQSSSEADPFW-VTLTPRS 81
Qy 63 YLTRIYIWIGLR-VON-----KGPCSSISYENLVDPCECFWVSBDTRLREMFKYDCEQGS 117
Db 82 LKTDLVWIGLKNINQSCYKMWKSDGTLYDYKXMRQFEC-LVSR-TYNNELMSHDCGTTYS 139
Qy 118 PICKP 122
Db 140 FVCKP 144

RESULT 41
ABA4 TRIAB STANDARD; PRT; 123 AA.
ID ABA4_TRIAB

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RESULT 42
06XST3 PRELIMINARY; PRT; 152 AA.
ID 06XST3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE C-type lectin CTU-5 (fragment).
OS Bitis arietans (African puff adder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OC NCB1_TaxID=8692;
RN NCB1_TaxID=8692;
RX SEQUENCE FROM N.A.
RA Harrison R.A., Oliver J.L., Haason S.S., Theakston D.R.D.G.;

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RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY254327; AAQ01208.1; -.
DR HSP; O9H8F0; 1K9J.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITSAF.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT NON TER.
SQ SEQUENCE 152 AA; 17254 MW; 78AB99D138108149 CRC64;

Query Match
Best Local Similarity 36.2%; Score 251.5; DB 2; Length 152;
Matches 48; Conservative 27; Mismatches 42; Indels 13; Gaps 3;

QY 1 DLECPGMSSTRYCYKPKKQEMTWASARPCSGQAKGHLISVETALASFDVNVLYAN 60
DB 24 DQCESEWASAYQHCYRAFKYKSVAKERFCWEQANDHLVSIOSIKANFAKLVSG- 82
QY 61 KEYLRYVYIGLRVONKQGPCSS-----ISYENLVDPFE--CFWVSRDTLREMFYD 111
DB 83 ---IAYVIGLRDRKKEQCTSEWNGSKVTVYVNRGEGSONCVLAIWGFKNWNTD 139
QY 112 CEQOHSFICK 121
DB 140 CASHNPFVCK 149

RESULT 43
Q91AM0 PRELIMINARY; PRT; 146 AA.
ID Q91AM0;
AC Q91AM0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Agkiscutacin B chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
RA Liu J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176421; AAF26287.1; -.
DR HSP; P22030; 1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITSAF.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16726 MW; 7360B6D6864111BB CRC64;

Query Match
Best Local Similarity 35.9%; Score 249.5; DB 2; Length 146;
Matches 53; Conservative 20; Mismatches 43; Indels 9; Gaps 5;

QY 3 ECPSSGMSSTRYCYKPKKQEMTWASARPCSGQAKGHLISVETALASFDVNVLYANKE 62
DB 24 DCPSSMSSEYEGHCYRPFDEPKTWADAEKFCQOHSGLASHSSSEADFV--VITLTPS 81
QY 63 YLTRYIWIQGLR-VON---KQPCSSISYENLVDPFEGWASRDRLRWPFVDEQOQS 117
DB 82 LKTDLWVIGLKNINIGCTWKKSDGTLDYDRROPEC-LVSR-IYNNEMLSMDGTTCS 139

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QY 118 PICKF 122
DB 140 FVCKF 144

RESULT 44
CVXB CRODU
ID CVXB CRODU STANDARD; PRT; 148 AA.
AC 093427;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Convulxin beta precursor (CVX beta).
OS Crocalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC TISSUE=Venom gland;
RX MEDLINE=98324301; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
RT aggregating protein from Crocalus durissus terrificus venom.";
RL Biochem. J. 333:389-393(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 24-148.
RX PubMed=14521935; DOI=10.1016/j.bbrc.2003.09.032;
RA Murakami M.T., Zela S.P., Gava L.M., Michelen-Duarte S.,
RA Cincira A.C.O., Arni R.K.;
RT "Crystal structure of the platelet activator convulxin, a disulfide-
RT linked alpha4beta4 cyclic tetramer from the venom of Crocalus durissus
RT terrificus.";
RL Biochem. Biophys. Res. Commun. 310:478-482(2003).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 25-148.
RX PubMed=14684891;
RA Batuwangala T., Leduc M., Gibbins J.M., Bon C., Jones E.Y.;
RT "Structure of the snake-venom toxin convulxin.",
RL Acta Crystallogr. D 60:46-53(2004).
CC -!- FUNCTION: Binds to the platelet and collagen receptor,
CC glycoprotein VI (GPVI).
CC -!- SUBUNIT: Heterooctamer of four alpha chains and four beta chains;
CC disulfide-linked.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Y16349; CAA76182.1; -.
DR EMBL; AF541881; AAQ11362.1; -.
DR PDB; 1UUR; X-ray; C/D=24-148.
DR PDB; 1UOS; X-ray; B/D=23-148.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO1504; PNCREATITSAF.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Lectin; Signal.

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FT SIGNAL 1 23
FT CHAIN 24 148 Convulxin beta.
FT DOMAIN 34 148 C-type lectin.
FT DISULFID 26 26 Interchain (with C-158 in alpha chain).
FT DISULFID 27 38
FT DISULFID 55 144
FT DISULFID 100 100 Interchain (with C-104 in alpha chain).
FT DISULFID 121 136
FT DISULFID 131 113
FT CONFLICT 148 148 K -> E (in Ref. 2).
FT CONFLICT 148 148 A -> V (in Ref. 2).
SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 35.8%; Score 249.5; DB 1; Length 148;
Best Local Similarity 41.3%; Pred. No. 2,3e-18;
Matches 52; Conservative 17; Mismatches 44; Indels 13; Gaps 5;

QY 4 CPBGNSSTDRYCYKPPKQEMTWASAEKFCSEQAKGHLISVETALASFYDNYLYANKE 63
DB 27 CPBHWSSYDRYCYKVFQEMTWADAEKFCQHGSHLVFSHTEBVDV--VYMTQSL 84
QY 64 LTRFYIIGLRVONKQGPC-----SSISYENLVDPPECEMWSRDRRLREMFKYDCEQH 116
DB 85 KSTFFWIG--ANNINWKNQMSDGTIKPEYKEMHEEFEC-LISR-TFDNQMLSAPCSDTY 140
QY 117 SFICKP 122
DB 141 SFVCKF 146

RESULT 45
Q8J1W1 PRELIMINARY; PRT; 146 AA.
AC Q8J1W1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Agkiscutacin B-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxId=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091756; AAM22785.1; -
DR PIR; JC7135; JC7135.
DR HSP; O93427; IUMR.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAF.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16740 MW; 6260B6D68741317C CRC64;

Query Match 35.8%; Score 248.5; DB 2; Length 146;
Best Local Similarity 42.4%; Pred. No. 2,9e-18;
Matches 53; Conservative 20; Mismatches 43; Indels 9; Gaps 5;

QY 3 ECPSGWSSTDRYCYKPPKQEMTWASAEKFCSEQAKGHLISVETALASFYDNYLYANKE 62
DB 24 DCPSEWSYSGHCHYKPPDEPKTWADAEKFCQHGSHLVFSHSEBVDV--VTLTPPS 81
QY 63 YLRFYIIGLR-VON-----KGPPSSSYENLVDPPECEMWSRDRRLREMFKYDCEQH 117
DB 82 LKTDLVWIGLKNINWGNCKYKMSDGTIKDYDMREQFEC-LVSR-TVNNWLSMDCGTTCS 139
QY 118 FICKP 122
DB 141 FICKP 122

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DB 140 FVCKP 144

RESULT 46
Q7IRP8 PRELIMINARY; PRT; 148 AA.
AC Q7IRP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stejaggregin-A beta chain-3.
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxId=39682;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Venom gland;
RA Lee W.-H., Liu H., Zhang Y.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354927; AAO15169.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAF.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 148 AA; 16966 MW; FBEC0046C3642524 CRC64;

Query Match 35.5%; Score 246.5; DB 2; Length 148;
Best Local Similarity 39.7%; Pred. No. 4.8e-18;
Matches 50; Conservative 20; Mismatches 43; Indels 13; Gaps 4;

QY 4 CPBGSSTDRYCYKPPKQEMTWASAEKFCSEQAKGHLISVETALASFYDNYLYANKE 63
DB 27 CPBGSSTDRYCYKPPKQEMTWADAEKFCQHGSHLVFSHSEBVDV--VYMTQSL 85
QY 64 LTRFYIIGLRVONKQGPCS-----ISYENLVDPPECEMWSRDRRLREMFKYDCEQH 116
DB 86 -LDFWVIGL--SNVWQCNSEMSDGTIKYKDMSESE--ISKTIENQMSRSCSRTH 140
QY 117 SFICKP 122
DB 141 YVCKP 146

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RESULT 47
Q6T7B5 PRELIMINARY; PRT; 157 AA.
AC Q6T7B5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-type lectin-3.
OS Bitis gabonica (Gaboon adder) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxId=8694;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Venom gland;
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Harrison J., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429479; AAR06853.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; Lectin_C; 1.

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DR InterPro; IPR001304; lectin\_C.  
DR InterPro; IPR003990; pancreatis\_ac.  
DR Pfam; PF00059; lectin\_C; 1.  
DR PRINTS; PR01504; PNCREATITSAP.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
SQ SEQUENCE 148 AA; 16936 MW; E49BBCA03A0A53F CRC64;

Query Match 34.9%; Score 242.5; DB 2; Length 148;  
Best Local Similarity 38.9%; Pred. No. 1,3e-17;  
Matches 49; Conservative 20; Mismatches 44; Indels 13; Gaps 4;

Qy	4	CPSGMSSTDRYCYKPFKQENTWASAEKFCSEQAKGHLISVETALASPVNDVLYANKEY	63
Db	27	CPFGMSYDLYCYKVFQGNMTDAEKFCTEQHTGSHLVSFHSSEADFVNMVTPILK-	85
Qy	64	LTRYTWIGLRVQNKQPCSS-----ISYENLVDPFECFVNSRDRRLREWFKVDCEQCH	116
Db	86	-LDFVWIGL--SNVMNQCNSEMSDGTGLDYKDMWSESEC--IASKTVENQNMWTKSCSRTH	140
Qy	117	SFICKP	122
Db	141	YVCKP	146

Search completed: May 2, 2005, 16:01:51  
Job time : 71 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 2, 2005, 16:01:56 ; Search time 56 Seconds  
(Without alignments)  
749,489 Million cell updates/sec

Title: US-10-749-387-1

Perfect score: 695  
Sequence: 1 DDECSGMSSTRVYCYKPKF.....WFKVDCQHSFICKFTRPR 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	695	100.0	126	9	US-09-969-763-1 Sequence 1, Appl1
2	695	100.0	126	9	US-10-749-387-1 Sequence 1, Appl1
3	684	98.4	149	9	US-09-969-763-3 Sequence 3, Appl1
4	684	98.4	149	16	US-10-749-387-3 Sequence 3, Appl1
5	542	78.0	110	9	US-09-969-763-10 Sequence 10, Appl1
6	542	78.0	110	16	US-10-749-387-10 Sequence 10, Appl1
7	361.5	52.0	158	9	US-09-929-230-11 Sequence 11, Appl1
8	361.5	52.0	158	14	US-10-326-420-11 Sequence 11, Appl1
9	316.5	45.5	144	9	US-09-929-230-8 Sequence 8, Appl1
10	316.5	45.5	144	14	US-10-326-420-8 Sequence 8, Appl1
11	314.5	45.3	152	9	US-09-929-230-5 Sequence 5, Appl1
12	314.5	45.3	152	14	US-10-326-420-5 Sequence 5, Appl1
13	271.5	39.1	129	10	US-09-938-114-2 Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-09-969-763-1  
; Sequence 1, Application US/09969763  
; Publication No. US20020198363A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUCHI, NAOYUKI  
; APPLICANT: KITO, MORTIAZU  
; APPLICANT: KAWAHARA, TAKASHI  
; APPLICANT: FUTARI, FUMIE  
; APPLICANT: ISHIKAWA, KOIKI  
; APPLICANT: SUZUKI, EIICHIRO  
; APPLICANT: GONDOH, KEIYO  
; APPLICANT: SHIMBA, NOBUHISA  
; APPLICANT: YAMADA, NAOYUKI  
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TI  
; FILE REFERENCE: 214760US0

14	184.5	26.5	151	9	US-09-929-230-2	Sequence 2, Appl1
15	184.5	26.5	151	14	US-10-326-420-2	Sequence 2, Appl1
16	168	24.2	166	10	US-09-997-003-30	Sequence 30, Appl1
17	168	24.2	166	10	US-09-997-003-43	Sequence 43, Appl1
18	168	24.2	166	16	US-10-734-564-2	Sequence 2, Appl1
19	168	24.2	166	16	US-10-734-564-4	Sequence 4, Appl1
20	168	24.2	174	9	US-09-925-301-1182	Sequence 1182, Ap
21	164.5	23.7	175	15	US-10-028-248A-112	Sequence 112, App
22	164.5	23.7	175	15	US-10-107-782-112	Sequence 112, App
23	157.5	22.7	175	15	US-10-028-248A-111	Sequence 111, App
24	157.5	22.7	175	15	US-10-107-782-111	Sequence 111, App
25	154.5	22.2	175	15	US-10-028-248A-110	Sequence 110, App
26	154.5	22.2	175	15	US-10-107-782-110	Sequence 110, App
27	153.5	22.1	175	14	US-10-316-761-3	Sequence 3, Appl1
28	153.5	22.1	175	15	US-10-434-906-1	Sequence 1, Appl1
29	153.5	22.1	175	15	US-10-028-248A-109	Sequence 109, App
30	153.5	22.1	175	15	US-10-107-782-109	Sequence 109, App
31	153.5	22.1	183	9	US-09-925-301-1013	Sequence 1013, Ap
32	148.5	21.4	175	9	US-09-978-295A-452	Sequence 452, App
33	148.5	21.4	175	9	US-09-978-697-452	Sequence 452, App
34	148.5	21.4	175	9	US-09-978-192A-452	Sequence 452, App
35	148.5	21.4	175	9	US-09-999-832A-452	Sequence 452, App
36	148.5	21.4	175	10	US-09-978-189-452	Sequence 452, App
37	148.5	21.4	175	10	US-09-978-608A-452	Sequence 452, App
38	148.5	21.4	175	10	US-09-978-585A-452	Sequence 452, App
39	148.5	21.4	175	10	US-09-978-191A-452	Sequence 452, App
40	148.5	21.4	175	10	US-09-978-403A-452	Sequence 452, App
41	148.5	21.4	175	10	US-09-978-564A-452	Sequence 452, App
42	148.5	21.4	175	10	US-09-999-833A-452	Sequence 452, App
43	148.5	21.4	175	10	US-09-981-915A-452	Sequence 452, App
44	148.5	21.4	175	10	US-09-978-824-452	Sequence 452, App
45	148.5	21.4	175	10	US-09-918-585A-452	Sequence 452, App
46	148.5	21.4	175	10	US-09-999-834A-452	Sequence 452, App
47	148.5	21.4	175	10	US-09-978-423A-452	Sequence 452, App
48	148.5	21.4	175	10	US-09-978-193A-452	Sequence 452, App
49	148.5	21.4	175	10	US-09-999-830A-452	Sequence 452, App
50	148.5	21.4	175	10	US-09-978-757A-452	Sequence 452, App
51	148.5	21.4	175	10	US-09-978-187B-452	Sequence 452, App
52	148.5	21.4	175	10	US-09-978-643A-452	Sequence 452, App
53	148.5	21.4	175	10	US-09-978-378A-452	Sequence 452, App
54	148.5	21.4	175	10	US-09-978-289A-452	Sequence 452, App
55	148.5	21.4	175	10	US-09-978-188A-452	Sequence 452, App
56	148.5	21.4	175	10	US-09-978-681A-452	Sequence 452, App
57	148.5	21.4	175	10	US-09-978-194A-452	Sequence 452, App
58	148.5	21.4	175	10	US-09-999-829A-452	Sequence 452, App
59	148.5	21.4	175	10	US-09-978-299A-452	Sequence 452, App
60	148.5	21.4	175	10	US-09-978-544A-452	Sequence 452, App
61	148.5	21.4	175	10	US-09-978-662A-452	Sequence 452, App
62	148.5	21.4	175	10	US-09-978-802A-452	Sequence 452, App
63	148.5	21.4	175	11	US-09-999-831A-452	Sequence 452, App
64	148.5	21.4	175	13	US-10-052-566-424	Sequence 424, App
65	148.5	21.4	175	14	US-10-174-590-424	Sequence 424, App

;; CURRENT APPLICATION NUMBER: US/09/969,763  
;; CURRENT FILING DATE: 2000-10-25  
;; PRIOR APPLICATION NUMBER: JP 2000-305279  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 126  
;; TYPE: PRF  
;; ORGANISM: Crocotalus horridus  
US-09-969-763-1

Query Match 100.0%; Score 695; DB 9; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 60  
DB 1 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 60

QY 61 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 120  
DB 61 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 120

QY 121 KFTRRP 126  
DB 121 KFTRRP 126

RESULT 2  
US-10-749-387-1  
; Sequence 1, Application US/10749387  
; Publication No. US20040161822A1  
; GENERAL INFORMATION:

;; APPLICANT: FUKUCHI, NAOYUKI  
;; APPLICANT: KITO, MORIKAZU  
;; APPLICANT: KAYAHARA, TAKASHI  
;; APPLICANT: FUTAKI, FUMIE  
;; APPLICANT: ISHIKAWA, KOHKI  
;; APPLICANT: SUZUKI, EIICHIRO  
;; APPLICANT: GONDOH, KEIKO  
;; APPLICANT: SHIMBA, NOBUHISA  
;; APPLICANT: YAMADA, NAOYUKI  
;; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT  
;; FILE REFERENCE: 214760USO  
;; CURRENT APPLICATION NUMBER: US/10/749,387  
;; CURRENT FILING DATE: 2004-01-02  
;; PRIOR APPLICATION NUMBER: US/09/969,763  
;; PRIOR FILING DATE: 2000-10-25  
;; PRIOR APPLICATION NUMBER: JP 2000-305279  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 126  
;; TYPE: PRF  
;; ORGANISM: Crocotalus horridus  
US-10-749-387-1

Query Match 100.0%; Score 695; DB 16; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 60  
DB 1 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 60

QY 61 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 120  
DB 61 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 120

QY 121 KFTRRP 126  
DB 121 KFTRRP 126

DB 121 KFTRRP 126

RESULT 3  
US-09-969-763-3  
; Sequence 3, Application US/09969763  
; Publication No. US20020198363A1  
; GENERAL INFORMATION:

;; APPLICANT: FUKUCHI, NAOYUKI  
;; APPLICANT: KITO, MORIKAZU  
;; APPLICANT: KAYAHARA, TAKASHI  
;; APPLICANT: FUTAKI, FUMIE  
;; APPLICANT: ISHIKAWA, KOHKI  
;; APPLICANT: SUZUKI, EIICHIRO  
;; APPLICANT: GONDOH, KEIKO  
;; APPLICANT: SHIMBA, NOBUHISA  
;; APPLICANT: YAMADA, NAOYUKI  
;; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT  
;; FILE REFERENCE: 214760USO  
;; CURRENT APPLICATION NUMBER: US/09/969,763  
;; CURRENT FILING DATE: 2000-10-25  
;; PRIOR APPLICATION NUMBER: JP 2000-305279  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 149  
;; TYPE: PRF  
;; ORGANISM: Crocotalus horridus  
US-09-969-763-3

Query Match 98.4%; Score 684; DB 9; Length 149;  
Best Local Similarity 98.4%; Pred. No. 7.4e-71;  
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 60  
DB 24 DLECPGMSSTDRYCYKPFQEMTWASAEFCEQAKGHLISVETALASFDVNLVYN 83

QY 61 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 120  
DB 84 KEYLTRYIWIIGLRYVQKGGPCSSISENLYDPECFMWSRDTLRLEMFVDCQOHSFIC 143

QY 121 KFTRRP 126  
DB 144 KFTRRP 149

RESULT 4  
US-10-749-387-3  
; Sequence 3, Application US/10749387  
; Publication No. US20040161822A1  
; GENERAL INFORMATION:

;; APPLICANT: FUKUCHI, NAOYUKI  
;; APPLICANT: KITO, MORIKAZU  
;; APPLICANT: KAYAHARA, TAKASHI  
;; APPLICANT: FUTAKI, FUMIE  
;; APPLICANT: ISHIKAWA, KOHKI  
;; APPLICANT: SUZUKI, EIICHIRO  
;; APPLICANT: GONDOH, KEIKO  
;; APPLICANT: SHIMBA, NOBUHISA  
;; APPLICANT: YAMADA, NAOYUKI  
;; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT  
;; FILE REFERENCE: 214760USO  
;; CURRENT APPLICATION NUMBER: US/10/749,387  
;; CURRENT FILING DATE: 2004-01-02  
;; PRIOR APPLICATION NUMBER: US/09/969,763  
;; PRIOR FILING DATE: 2000-10-25  
;; PRIOR APPLICATION NUMBER: JP 2000-305279  
;; PRIOR FILING DATE: 2000-10-04  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 3

LENGTH: 149  
TYPE: PRT  
ORGANISM: Crocalus harridus  
US-10-749-387-3

Query Match 98.4%; Score 684; DB 16; Length 149;  
Best Local Similarity 98.4%; Pred. No. 7, 4e-71;  
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIECPGSGMSTRYCYKPKPKQEMTWASARFCSQAKGHLISVETALASFDVNLVYAN 60  
DB 24 DIECPGSGMSYDRYCYKPKQEMTWADARFCSQAKGHLISVETALASFDVNLVYAN 83  
QY 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 120  
DB 84 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 143  
QY 121 KETRRR 126  
DB 144 KETRRR 149

RESULT 5  
US-09-969-763-10  
Sequence 10, Application US/09969763  
Publication No. US20020198363A1

GENERAL INFORMATION:  
APPLICANT: FUKUCHI, NAOYUKI  
APPLICANT: KITO, MORIKAZU  
APPLICANT: KAYAHARA, TAKASHI  
APPLICANT: FUTAKI, FUMIE  
APPLICANT: ISHIKAWA, KOHKI  
APPLICANT: SUZUKI, EICHIRO  
APPLICANT: GONDOH, KEIKO  
APPLICANT: SHIMBA, NOBUHISA  
APPLICANT: YAMADA, NAOYUKI  
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING T  
FILE REFERENCE: 214760USO  
CURRENT APPLICATION NUMBER: US/09/969,763  
PRIOR FILING DATE: 2000-10-25  
PRIOR APPLICATION NUMBER: JP 2000-305279  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 10  
LENGTH: 110  
TYPE: PRT  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-09-969-763-10

Query Match 78.0%; Score 542; DB 9; Length 110;  
Best Local Similarity 81.7%; Pred. No. 1, 3e-54;  
Matches 103; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 DIECPGSGMSTRYCYKPKPKQEMTWASARFCSQAKGHLISVETALASFDVNLVYAN 60  
DB 1 DIECPGSGMSYDRYCYKPKQEMTWADARFCSQAKGHLISVETALASFDVNLVYAN 60  
QY 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 120  
DB 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 104  
QY 121 KETRRR 126  
DB 105 KETRRR 110

RESULT 6  
US-10-749-387-10  
Sequence 10, Application US/10749387  
Publication No. US20040161822A1

GENERAL INFORMATION:  
APPLICANT: FUKUCHI, NAOYUKI  
APPLICANT: KITO, MORIKAZU  
APPLICANT: KAYAHARA, TAKASHI  
APPLICANT: FUTAKI, FUMIE  
APPLICANT: ISHIKAWA, KOHKI  
APPLICANT: SUZUKI, EICHIRO  
APPLICANT: GONDOH, KEIKO  
APPLICANT: SHIMBA, NOBUHISA  
APPLICANT: YAMADA, NAOYUKI  
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING T  
FILE REFERENCE: 214760USO  
CURRENT APPLICATION NUMBER: US/10/749,387  
PRIOR FILING DATE: 2004-01-02  
PRIOR APPLICATION NUMBER: US/09/969,763  
PRIOR FILING DATE: 2000-10-25  
PRIOR APPLICATION NUMBER: JP 2000-305279  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 10  
LENGTH: 110  
TYPE: PRT  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-10-749-387-10

Query Match 78.0%; Score 542; DB 16; Length 110;  
Best Local Similarity 81.7%; Pred. No. 1, 3e-54;  
Matches 103; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 DIECPGSGMSTRYCYKPKPKQEMTWASARFCSQAKGHLISVETALASFDVNLVYAN 60  
DB 1 DIECPGSGMSYDRYCYKPKQEMTWADARFCSQAKGHLISVETALASFDVNLVYAN 60  
QY 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 120  
DB 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 104  
QY 121 KETRRR 126  
DB 105 KETRRR 110

RESULT 7  
US-09-929-230-11  
Sequence 11, Application US/09929230  
Patent No. US20020161203A1

GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Bishop, Paul D.  
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS  
FILE REFERENCE: 00-72  
CURRENT APPLICATION NUMBER: US/09/929,230  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Sistrurus miliarius  
US-09-929-230-11

Query Match 52.0%; Score 361.5; DB 9; Length 158;  
Best Local Similarity 50.4%; Pred. No. 1, 6e-33;  
Matches 66; Conservative 21; Mismatches 35; Indels 9; Gaps 2;

QY 1 DIECPGSGMSTRYCYKPKPKQEMTWASARFCSQAKGHLISVETALASFDVNLVYAN 60  
DB 24 DFNCPGSGMFPAYDOYCYRVYIKRLKTWDDARFCSQAKGHLASVENDEDAVFLAOLVYAN 83  
QY 61 KEYLTRYIWIIGLRVQNKGPCCSSISYENLVDPFECFMVSRDTRLREMFVDCQGHSPFC 111







Db 90 ESGTDDFNWIGLHDPKRRMWSGSLVSYKSWGIGAPSSVNPQYCVSLTSTGTFORK 149  
Qy 108 FKVDCEQHSFICKF 122  
Db 150 KDVPCEDKFSFVCKF 164

## RESULT 19

US-10-734-564-4  
; Sequence 4, Application US/10734564  
; Publication No. US20040157278A1  
; GENERAL INFORMATION:  
; APPLICANT: Christopher C Burgess et al  
; TITLE OF INVENTION: Detection Methods Using TIMP1  
; FILE REFERENCE: 1657/2012  
; CURRENT APPLICATION NUMBER: US/10/734,564  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-734-564-4

Query Match 24.2%; Score 168; DB 16; Length 166;  
Best Local Similarity 31.1%; Pred. No. 4.1e-11;  
Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

Qy 2 LKCPGMSSTDRCYKPFQKQMTWASAEFRCSEQAKGHLSTVETALASFDVNVLYANK 61  
Db 34 ISCPGNTNRYSCYCFNDRBTWVDALYC-QNNNSGNLVSLTQAEQAFVASLI---K 89  
Qy 62 EYLTR--YIWIGLRVONKGO-----PCSSISYE-----NLVDPCECFMWSRDTLRKM 107  
Db 90 ESGTDDFNWIGLHDPKRRMWSGSLVSYKSWGIGAPSSVNPQYCVSLTSTGTFORK 149  
Qy 108 FKVDCEQHSFICKF 122  
Db 150 KDVPCEDKFSFVCKF 164

## RESULT 20

US-09-925-301-1182  
; Sequence 1182, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1182  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1182

Query Match 24.2%; Score 168; DB 9; Length 174;  
Best Local Similarity 31.1%; Pred. No. 4.4e-11;  
Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

Qy 2 LKCPGMSSTDRCYKPFQKQMTWASAEFRCSEQAKGHLSTVETALASFDVNVLYANK 61  
Db 42 ISCPGNTNRYSCYCFNDRBTWVDALYC-QNNNSGNLVSLTQAEQAFVASLI---K 97

Qy 62 EYLTR--YIWIGLRVONKGO-----PCSSISYE-----NLVDPCECFMWSRDTLRKM 107  
Db 98 ESGTDDFNWIGLHDPKRRMWSGSLVSYKSWGIGAPSSVNPQYCVSLTSTGTFORK 157  
Qy 108 FKVDCEQHSFICKF 122  
Db 158 KDVPCEDKFSFVCKF 172

## RESULT 21

US-10-028-248A-112  
; Sequence 112, Application US/10028248A  
; Publication No. US20030235882A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Vermet, Corine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Malyankar, Ute1  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Gangoli, Esha  
; APPLICANT: Miller, Charles  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Kerkuda, Ramesh  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Zethusen, Bryan  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Coleman, Steven  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Stone, David  
; APPLICANT: Sclote, Paul  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Rothenberg, Mark  
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods  
; FILE REFERENCE: 21402-222  
; CURRENT APPLICATION NUMBER: US/10/028,248A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311266  
; PRIOR FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 112  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-028-248A-112

Query Match 23.7%; Score 164.5; DB 15; Length 175;  
Best Local Similarity 30.0%; Pred. No. 1.1e-10;  
Matches 42; Conservative 20; Mismatches 57; Indels 21; Gaps 4;

Qy 2 LKCPGMSSTDRCYKPFQKQMTWASAEFRCSEQAKGHLSTVETALASFDVNVLYANK 60  
Db 38 ISCPGMSQYGYCYCALFIPOTWDAELAC-QKRPGLVSLVLSAELASFLSNVKTG 96  
Qy 61 KEYLFRYIWIGLRVONKGOPCSSISYE-----NLVDPCECFMWSRDTLR 103

Db 97 NSY--QYTWIGLHPTLGAEPNGGWEWSNNDVMNYFNMERNPSTALDRACGSLSRASG 154  
QY 104 LREWFVDCQOHSFICKET 123  
Db 155 FLKWRDMTCVXLPHYCKET 174

## RESULT 22

US-10-107-782-112  
; Sequence 112, Application US/10107782  
; Publication No. US20040018970A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Casman, Stacie  
; APPLICANT: Coleman, Steve,  
; APPLICANT: Edinger, Shlomlt,  
; APPLICANT: Gangolli, Esha,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Li, Li,  
; APPLICANT: Liu, Xiaohong,  
; APPLICANT: Malyankar, Uriel,  
; APPLICANT: Miller, Charles,  
; APPLICANT: Millet, Isabelle,  
; APPLICANT: Patturajan, Meera,  
; APPLICANT: Rothenberg, Mark,  
; APPLICANT: Sciore, Paul,  
; APPLICANT: Shenoy, Suresh,  
; APPLICANT: Shimkets, Richard,  
; APPLICANT: Si, Jingsheng,  
; APPLICANT: Smithson, Glenda,  
; APPLICANT: Spytek, Kimberly,  
; APPLICANT: Stone, David,  
; APPLICANT: Taupier, Raymond, Jr.,  
; APPLICANT: Tchernev, Velizar,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Zerhusen, Brian  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 21402-222CIP  
; CURRENT APPLICATION NUMBER: US/10/107,782  
; FILE REFERENCE: 21402-222CIP  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 10/028,248  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/279,344  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: CuraSeqdist version 0.1  
; SEQ ID NO 112  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-107-782-112

Query Match 23.7%; Score 164.5; DB 15; Length 175;  
Best Local Similarity 30.0%; Pred. No. 1.1e-10;  
Matches 42; Conservative 20; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGWSSTDRYCYKPFKQEMTWASAEFPCSEQAKGHLISVETALASFDVN-VLYAN 60  
Db 38 ISCPKSGQAGSYCYALFQIPQTFPDAELAC-QKRPBGHLVSVLVNVAEASFLASMTVARTG 96  
QY 61 KEYLTRYIWTGLRVQNKGPCSSISYE-----NLVDPFECFVNSDTR 103

Db 97 NSY--QYTWIGLHPTLGAEPNGGWEWSNNDVMNYFNMERNPSTALDRACGSLSRASG 154  
QY 104 LREWFVDCQOHSFICKET 123  
Db 155 FLKWRDMTCVXLPHYCKET 174

## RESULT 23

US-10-028-248A-111  
; Sequence 111, Application US/10028248A  
; Publication No. US20030235882A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Vernet, Corine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Miller, Charles  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Coleman, Steven  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Edinger, Shlomlt  
; APPLICANT: Stone, David  
; APPLICANT: Sciore, Paul  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Rothenberg, Mark  
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods of Use Thereof  
; FILE REFERENCE: 21402-222  
; CURRENT APPLICATION NUMBER: US/10/028,248A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 111  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-028-248A-111

Query Match 22.7%; Score 157.5; DB 15; Length 175;  
Best Local Similarity 30.2%; Pred. No. 7.2e-10;  
Matches 42; Conservative 21; Mismatches 57; Indels 19; Gaps 5;

QY 2 LBCPSGWSSTDRYCYKPFKQEMTWASAEFPCSEQAKGHLISVETALASFDVN-VLYAN 61  
Db 38 ISCPKSGQAGSYCYALFQIPQTFPDAELACQKRPBGHLVSVLVNVAEASFLASMTVARTG 95  
QY 62 EYLTRYIWTGLRVQNKGPCSS-----ISYEN-----LVDPFECFVNSDTR 104  
Db 96 GNSYQYTWIGLHPTLGAEPNGGWEWSNNDVMNYFNMERNPSTALDRACGSLSRASG 155



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QY      105 REMFKVDCEQHSFICKFT 123
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DB      156 LRWRDTTCEVKLPYVCKFT 174
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RESULT 24  
US-10-107

; Sequence 111, Application US/10107782  
; Publication No. US20040018970A1

; GENERAL INFORMATION:

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ORGANISM: Homo sapiens  
US-10-107-782-111

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Query Match 22.7%; Score 157.5; DB 15; Length 175;
Best Local Similarity 30.2%; Read No. 7,2e-10;
Matches 42; Conservative 21; Mismatches 57; Indels 19; Gaps 5

QY      2  LCPSGMSDTRYCYKPFQKQENTWASAEFCEQAKGHLSVETALEASPYDNLVYANK 61
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       38  ISCPGSOAYGSCYALFQIPQTFDAELACQKPE-GHLSVILNVAEASFLASWY-KNT 95
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      62  EYLTYITIGLRVQN-KQGPCSS-----ISTEN-----LVDPPECIMVSRDRL 104
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Db 96 GNSYQYTWYGLMDPTLGGSPNCGMWEWNSNDIMYVNMERNPSTALDRGFCGSLRSRSGF 155

Qy 105 REMFKVDCEQHSFICKFT 123

Db 156 LRMRDTTCVRLPYVCKFT 174

RESULT 25  
US-10-028-248A-110

; Sequence 110, Application US/10028248A  
; Publication No. US20030235882A1  
; JOURNAL INFORMATION

APPLICANT: Shimket

```

: APPLICANT: Patrice Jean, Meera
: APPLICANT: Vermet, Corine
: APPLICANT: Casman, Stacie
: APPLICANT: Malyankar, Uriel
: APPLICANT: Shenoy, Suresh
: APPLICANT: Spytek, Kimberly
: APPLICANT: Gangoli, Esna
: APPLICANT: Miller, Charles
: APPLICANT: Boldog, Ferenc
: APPLICANT: Li, Li
: APPLICANT: Taupier Jr, Raymond J
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Smithson, Glenda
: APPLICANT: Zernusen, Bryan
: APPLICANT: Liu, Xiaohong
: APPLICANT: Coleman, Steven
: APPLICANT: Tchernov, Velizar
: APPLICANT: Si, Jingsheng
: APPLICANT: Edinger, Shlomit
: APPLICANT: Stone, David
: APPLICANT: Sciore, Paul
: APPLICANT: Miller, Isabelle
: APPLICANT: Rothenberg, Mark
: TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods c
: TITLE OF INVENTION: Theoreof
: FILE REFERENCE: 21402-222
: CURRENT APPLICATION NUMBER: US/10/028,248A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/256619
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 60/262959
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/272408
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 60/285189
: PRIOR FILING DATE: 2001-04-20
: PRIOR APPLICATION NUMBER: 60/308039
: PRIOR FILING DATE: 2001-07-26
: PRIOR APPLICATION NUMBER: 60/311266
: PRIOR FILING DATE: 2001-08-09
: NUMBER OF SEQ ID NOS: 211
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 110
: LENGTH: 175
: TYPE: prt
: ORGANISM: Bos taurus
: US-10-028-248A-110

```

Query Match	22.2%	Score 154.5	DB 15	length 175
Best Local Similarity	30.2%	Pred. No. 1.6e-09		
Matches 42	Conservative 19	Mismatches 59	Indels 19	Gaps 4

```

Oy  2  LEEPSGSSNDRCYCPYFQEOENTMASAEFCSEQAKGHLLSVEFALAEASFEVDVLYANK  61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  38  ISCESSMAVRSHTCYALFTPKTMTMDADIAQ-QKRPGLHLYVLSGAESEFVAS-LVRNN  95

      62  EYLRITVITGLRQKNGQPCSSISYE-----NY-----DPFEGEMSRDRL  10
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      96  LNTQSDITGLHLDPTGSEPAKNGGEMWISNDVLTAVMETPDAIISFGYCGSLRSRSGY  15

```

QY 105 REMFKVDCQOHSFICKT 123  
DB 156 LKWRDHNCNLNLPYCKFT 174

## RESULT 26

US-10-107-782-110  
Sequence 110, Application US/10107782  
Publication No. US20040018970A1  
GENERAL INFORMATION:  
APPLICANT: Boldog, Ferenc,  
APPLICANT: Casman, Stacie  
APPLICANT: Colman, Steve,  
APPLICANT: Edinger, Shlomit,  
APPLICANT: Gangoli, Esha,  
APPLICANT: Kerkuda, Ramesh,  
APPLICANT: Li, Li,  
APPLICANT: Liu, Xiaohong,  
APPLICANT: Malvanekar, Uriel,  
APPLICANT: Miller, Charles,  
APPLICANT: Millet, Isabelle,  
APPLICANT: Patuturajan, Meera,  
APPLICANT: Rothenberg, Mark,  
APPLICANT: Sciore, Paul,  
APPLICANT: Skenoy, Suresh,  
APPLICANT: Shimkets, Richard,  
APPLICANT: Si, Jingsheng,  
APPLICANT: Smithson, Glenda,  
APPLICANT: Spytek, Kimberly,  
APPLICANT: Stone, David,  
APPLICANT: Taupier, Raymond, Jr.,  
APPLICANT: Tchernev, Velizar,  
APPLICANT: Vernet, Corine,  
APPLICANT: Zernhusen, Brian  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
FILE REFERENCE: 21402-222CIP  
CURRENT APPLICATION NUMBER: US/10107, 782  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 10/028, 248  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/256, 619  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/262, 959  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/272, 408  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: 60/285, 189  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/308, 039  
PRIOR FILING DATE: 2001-07-26  
PRIOR APPLICATION NUMBER: 60/311, 266  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/279, 344  
PRIOR FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: Curaseqdist version 0.1  
SEQ ID NO 110  
LENGTH: 175  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-107-782-110

Query Match 22.2%; Score 154.5; DB 15; Length 175;  
Best Local Similarity 30.2%; Pred. No. 1.6e-09;  
Matches 42; Conservative 19; Mismatches 59; Indels 19; Gaps 4;

QY 2 LBCPSGMSSTDRYCYKPFQEMTWSAERFCSEQAKGHLISVETALASFDVNLVYANK 61  
DB 38 ISCPSSGSMAYRSHCVLFTPKTMDADIAC-QKPSGHLVSLGAGSFSVAS-LVRNN 95  
QY 62 EYITRITWIGLRVONKQGPCSSISYE-----NLV-----DPFECFVMSDTRL 104  
DB 96 LNTQSDIWIGLHDPTEGSEANAGWEMISNDVNLVYAMETDPAISSPGCSLSRSSGY 155

QY 105 REMFKVDCQOHSFICKT 123  
DB 156 LKWRDHNCNLNLPYCKFT 174

## RESULT 27

US-10-316-761-3  
Sequence 3, Application US/10316761  
Publication No. US20030109004A1  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/316, 761  
FILING DATE: 10-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/822, 261  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36, 749  
REFERENCE/DOCKET NUMBER: PF-0251 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 262369  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-316-761-3

Query Match 22.1%; Score 153.5; DB 14; Length 175;  
Best Local Similarity 25.7%; Pred. No. 2.1e-09;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYKPFQEMTWSAERFCSEQAKGHLISVETALASFDVNLVY-N 60  
DB 38 IRCPKSKAYVSHCVLFTSPKSWTDADIAC-QKPSGNLVSLGAGSFSVSLVKSIG 96  
QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYE-----NLVDPFECFVMSRDPTR 103  
DB 97 NSY--SYTWIGLHDPTEGSEANAGWEMISNDVNLVYAMERNPITISSPGHCAISRSRTA 154  
QY 104 LREMKVDCQOHSFICKT 123  
DB 155 FLRMQVNCNVLNLPYCKFT 174

RESULT 28  
US-10-434-906-1

Sequence 1, Application US/10434906  
Publication No. US2003022000A1  
GENERAL INFORMATION:  
APPLICANT: William P. Van Antwerp  
TITLE OF INVENTION: IMMUNOPROTECTIVE METHODS FOR BETA CELL  
FILE REFERENCE: 130.59-US-01  
CURRENT APPLICATION NUMBER: US/10/434,906  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: 60/379,202  
PRIOR FILING DATE: 2002-05-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FaalSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 175  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-434-906-1

Query Match 22.1%; Score 153.5; DB 15; Length 175;  
Best Local Similarity 25.7%; Pred. No. 2.1e-09;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYFPKQEMTWASAEFCSEQAKGHLSTVETLAEAFVNDVLYA-N 60  
DB 38 ICPKSKAYGSHCYALFLSPKSWTDADLAC-OKRPSGNLVSLGAEGSFVSLVKSIG 96  
QY 61 KEYLTRYINIGLRVQNKQPCSSISYE-----NLVDPCECFMVRDTR 103  
DB 97 NSY--SYWIGLHDPQTEPNGEWESSSDVMYFAMERNPSTISSGHCSLSRSTA 154  
QY 104 LREWFVDCQCHSFCKFT 123  
DB 155 FLRMKDYNQVRLPYVCKFT 174

## RESULT 29

US-10-028-248A-109  
Sequence 109, Application US/10028248A  
Publication No. US20030235882A1  
GENERAL INFORMATION:

APPLICANT: Shimkets, Richard  
APPLICANT: Patuturajan, Meera  
APPLICANT: Vernet, Corine  
APPLICANT: Casman, Stacie  
APPLICANT: Malyanekar, Uriel  
APPLICANT: Shenoy, Suresh  
APPLICANT: Spytek, Kimberly  
APPLICANT: Gangolli, Beha  
APPLICANT: Miller, Charles  
APPLICANT: Boldog, Ferenc  
APPLICANT: Li, Li  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Smithson, Glenda  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Liu, Xiaohong  
APPLICANT: Coleman, Steven  
APPLICANT: Tchernen, Velizar  
APPLICANT: Si, Jingsheng  
APPLICANT: Edinger, Shlomil  
APPLICANT: Stone, David  
APPLICANT: Sciore, Paul  
APPLICANT: Millet, Isabelle  
APPLICANT: Rothenberg, Mark  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
FILE REFERENCE: 21402-222  
CURRENT APPLICATION NUMBER: US/10/028,248A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/256619  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/262959

PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/272408  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: 60/285189  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/308039  
PRIOR FILING DATE: 2001-07-26  
PRIOR APPLICATION NUMBER: 60/311266  
PRIOR FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 211  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 109  
LENGTH: 175  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-028-248A-109

Query Match 22.1%; Score 153.5; DB 15; Length 175;  
Best Local Similarity 25.7%; Pred. No. 2.1e-09;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYFPKQEMTWASAEFCSEQAKGHLSTVETLAEAFVNDVLYA-N 60  
DB 38 ICPKSKAYGSHCYALFLSPKSWTDADLAC-OKRPSGNLVSLGAEGSFVSLVKSIG 96  
QY 61 KEYLTRYINIGLRVQNKQPCSSISYE-----NLVDPCECFMVRDTR 103  
DB 97 NSY--SYWIGLHDPQTEPNGEWESSSDVMYFAMERNPSTISSGHCSLSRSTA 154  
QY 104 LREWFVDCQCHSFCKFT 123  
DB 155 FLRMKDYNQVRLPYVCKFT 174

## RESULT 30

US-10-107-782-109  
Sequence 109, Application US/10107782  
Publication No. US20040018970A1  
GENERAL INFORMATION:

APPLICANT: Boldog, Ferenc  
APPLICANT: Casman, Stacie  
APPLICANT: Coleman, Steve  
APPLICANT: Edinger, Shlomil  
APPLICANT: Gangolli, Beha  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: Liu, Xiaohong  
APPLICANT: Malyanekar, Uriel  
APPLICANT: Miller, Charles  
APPLICANT: Millet, Isabelle  
APPLICANT: Patuturajan, Meera  
APPLICANT: Rothenberg, Mark  
APPLICANT: Sciore, Paul  
APPLICANT: Shenoy, Suresh  
APPLICANT: Shimkets, Richard  
APPLICANT: Si, Jingsheng  
APPLICANT: Smithson, Glenda  
APPLICANT: Spytek, Kimberly  
APPLICANT: Stone, David  
APPLICANT: Taupier, Raymond, Jr.  
APPLICANT: Tchernen, Velizar  
APPLICANT: Vernet, Corine  
APPLICANT: Zerhusen, Brian  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
FILE REFERENCE: 21402-222CIP  
CURRENT APPLICATION NUMBER: US/10/107,782  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 10/028,248  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/256,619  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/262,959  
PRIOR FILING DATE: 2001-01-19

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; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 109
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-107-782-109
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Query Match      22.1%; Score 153.5; DB 15; Length 175;
Best Local Similarity 25.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;
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QY 2 LKCPGMSSTDRYCYKPFQEMTWASAEFCSEDAKGGHLLSVETALASFDNVLYA-N 60
DB 38 IICPKSKAYGSHCTALFTSPKSWTDADLAC-QKRPNGNLVSLGABGSPVSLVKSIG 96
QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYE-----NLVDFECFMYSRDTR 103
DB 97 NSY--SYWIGLHDPGTGTEPNEGGEWSSSDVMNFAMERNPSTISSPGHCASLSRSTA 154
QY 104 LREWFVDECEQHSFICKFT 123
DB 155 FLRMKDYNQNVLLPYVCKFT 174
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RESULT 31
US-09-925-301-1013
; Sequence 1013, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1013
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-925-301-1013
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Query Match      22.1%; Score 153.5; DB 9; Length 183;
Best Local Similarity 25.7%; Pred. No. 2.2e-09;
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;
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QY 2 LKCPGMSSTDRYCYKPFQEMTWASAEFCSEDAKGGHLLSVETALASFDNVLYA-N 60
DB 46 IICPKSKAYGSHCTALFTSPKSWTDADLAC-QKRPNGNLVSLGABGSPVSLVKSIG 104
QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYE-----NLVDFECFMYSRDTR 103
DB 105 NSY--SYWIGLHDPGTGTEPNEGGEWSSSDVMNFAMERNPSTISSPGHCASLSRSTA 162
QY 104 LREWFVDECEQHSFICKFT 123
DB 163 FLRMKDYNQNVLLPYVCKFT 182
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RESULT 32
US-09-978-295A-452
; Sequence 452, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavitt, Iyar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
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PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
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PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
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PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTRRCYCFPEQEMTWASABRFGCSBOAKGHLSTVETLAEAFVNVNYYA-N 60  
DB 38 ISCPKSKAYGSPCALFLSPKSWMDADLAC-QKPSGKLVSIVLSGABGSFVSLVR3IS 96  
QY 61 KEYLTRYIWIIGLRVQNGQPCSSISYE-----NLVDPFECFMRSDTR 103  
DB 97 NSY--SYIWIIGLHDPQSGEPDGDGWEWSSTDVNMYFAWEKXNPSTILNIGHGCSLSR5TG 154  
QY 104 LREWFVDCBQCHSFICKF 122  
DB 155 FLTKMDYNDACKLPYCKF 173

RESULT 33  
US-09-978-697-452  
Sequence 452, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvarolt, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT FILING DATE: 2001-10-16  
PRIOR FILING DATE: 2001-07-30  
PRIOR FILING DATE: 2001-07-30  
PRIOR FILING DATE: 1997-10-17  
PRIOR FILING DATE: 1997-10-17  
PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-03-20  
PRIOR FILING DATE: 1998-03-25  
PRIOR FILING DATE: 1998-03-25  
PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
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PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495



PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
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PRIOR APPLICATION NUMBER: 60/080194  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
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PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
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PRIOR APPLICATION NUMBER: 60/083495  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LECPSGWSSTRYCKPKKQEMTASARFQSEOKAGHLSVETALASFDVNLVA-N 60  
DB 38 ISCPKGSYAYGSPCTALTLSPKSWMDADLAC-QKRPSSKLVSIVLSGAGCSFVSSIVRSIS 96  
QY 61 KEYLFRYIMIGLRVONKQPCSSISYE-----NLVDPFECFVWSRPDR 103  
DB 97 NSY--SYIMWIGLHDTQSGSPEDGDGQWMSSTIDWNNYFAMENKPSITILNPGHGSLSRSTG 154  
QY 104 LREMFKVDCEQOHSFTCKF 122



DB : : : : :  
155 FLKMDYNDACKLPYVCKF 173

RESULT 35  
US-09-999-832A-452  
Sequence 452, Application US/09999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Aekhenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999, 832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/079656  
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PRIOR APPLICATION NUMBER: 60/083322  
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;; PRIOR APPLICATION NUMBER: 60/083495  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

Qy 2 LCPGSGMSRDRCYCFEFGQEMTWSAERFCSEQAAGHLLSVETLLEASFYDNTVYX-N 60  
Db 38 ISCPKSKAYGSPCTALFLSPKSWMDADLAC-QKRPSTVSLVSGAESFVSLVRSIS 96  
Qy 61 KEYLTRYIWIGLRVONKGPCCSISYE-----NLVDPFECFVWSRDR 103  
Db 97 NSY--SYIWIGLHDPQSGEPDGDGEMWSSTVWNTFAMEKNPSTILNCHGCSLSRSRG 154

Qy 104 LREMFKVDCEQOHSPICKF 122  
Db 155 FLKMKDYNCDAXLPYCKF 173

RESULT 36  
US-09-978-189-452  
; Sequence 452, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Fred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

Qy 2 LECPSGMSSTRDYCPFQOEWTAABRFSCEQAKGHLISVETLAEASPVQNVLYA-N 60  
Db 38 ISCPKSKAYGSPCYLFLSPKSMADADLAC-QKRSGLTVLSABESGFSVLSRSTIS 96  
Qy 61 KEYLTRYINIGLRVONKGPCCSSISYE-----NLVDPPECFMWRDTR 103  
Db 97 NSY--SYIWIIGLHDPQSGSEPDGDGWMGSSTDVNNYFAWEKKNPSTILNHCGLSRSTG 154



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC4  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09; Mismatches 57; Indels 21; Gaps 4;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 IECPSGWSSTDRYCYKPFQCEMTWASABRFSCEQAKGHLSEVPTLEASFVDNYLYA-N 60  
DB 38 ISCPFGSKAYGSPCYALFISPKSMDADLAC-QKRPSCGLVSLGABGSFVSSLVRSIS 96

QY 61 KEYLTRYTWIGLRVONKGGQPCSSISYE-----NLVDFEFCFVWSRDTTR 103  
DB 97 NSY--SYIWIIGHDHPQGSSEPDGDGWEWSSTDVWNYFAWEKNPSTILNGHCGSLRSRTG 154

QY 104 LREWFKVDEQGHSTFCKF 122  
DB 155 FLKMDVNDCAKLPIYCKF 173

RESULT 40  
US-09-978-403A-452  
; Sequence 452, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/080105  
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PRIOR FILING DATE:	1998-03-31
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PRIOR APPLICATION NUMBER:	60/083742
PRIOR FILING DATE:	1998-04-30

[illegible]

Query Match	21.4%	Score 148.5;	DB 10;	Length 175;
Best Local Similarity	25.9%	Pred. No. 8e-09;		
Matches	36;	Conservative	25;	Mismatches 57;
				Indels 21;
				Gaps 4;

[illegible]

RESULT 41  
US-09-978-564A-452  
: Sequence 452, Application US/09978564A  
: Publication NO. US20030050241A1  
: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Botstein, David  
: APPLICANT: Desnovers, Luc  
: APPLICANT: Eilat, Dan  
: APPLICANT: Ferrara, Napoleon  
: APPLICANT: Flivaroff, Ellen  
: APPLICANT: Fong, Sherman  
: APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/083742



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PRIOR FILING DATE: 1998-05-05  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09; Mismatches 57; Indels 21; Gaps 4;  
Matches 36; Conservative 25; Mismatch 57; Indel 21; Gap 4;

QY 2 LECPSGMSSTRDYCYKPKQEMTWASAEPCSEQAGHLLSVETALASFDVNLVYA-N 60  
DB 38 ISCPKSKAYGSPCYALFLSPKSMWDADLAC-QKPSGKLVSVLSGAESEFVSIVRSIS 96  
QY 61 KEVLTYYITIGLAVONKQGPCSSISYE-----NLVDPECFMWSRDT 103  
DB 97 NSY--SYIWIGLHDPPOGSEPPDDGDGWEWSSTDVWNYFAWEKNSPTILNPHCSLSRSTG 154  
QY 104 LREWFYKDCQOHSFICKF 122  
DB 155 FLKMKDYNCDAKLPYCKF 173

RESULT 42  
US-09-999-833A-452  
Sequence 452, Application US/09999833A  
Publication No. US20030054405A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105



APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
PRIOR FILING DATE: 2001-10-16  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGWSSTDRKCYCFKQEMTWASAEFCSEQAKGHLSTALASFDVNLVLA-N 60  
DB 38 ISCPKSKYVGSYALFLSPKSMWDADLAC-QKPSGKLVSTLGAEGSFVSLVRSIS 96  
QY 61 KEVLTYMIGLAVQKQGPCSSISYE-----NIVDPCECFMWSRDR 103  
DB 97 NST--SYIIGLHDPTQSGEPDGDGWSSTVDMNTFANEKPNSTILNPGHCSLSRSTG 154  
QY 104 LRFMFVDCQCHSFICKF 122  
DB 155 FLKMKDYNDAKLPYCKF 173

RESULT 44  
US-09-978-824-452

; Sequence 452, Application US/09978824  
; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon

;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gertsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
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;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gueney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Thomas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C14  
;; CURRENT APPLICATION NUMBER: US/09/978,824  
;; PRIOR FILING DATE: 2001-10-17  
;; PRIOR APPLICATION NUMBER: 09/918585  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.3%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTRDCYCPFKQEMTWASAEFCSQAKGHLSTVETALASFDVNLVA-N 60  
DB 38 ISCPKSKAYGSPDYALFSPKSMWDADLAC-OKRPSGKLVSVLGAGSGSFVSLVRSIS 96  
QY 61 KEVLTIRYIWIGLHVONKQPCSSISYE-----NLVDPCECFVNSHDT 103  
DB 97 NSY--SYIWGLDPPQSGSPDDGDGHEMSSTDYMNTPAMKNSSTILNPHCHCSLSSTG 154  
QY 104 LREMFVDCQOHSFICKF 122  
DB 155 FLKMKDYNDCAKLPYCKF 173

RESULT 45  
US-09-918-585A-452  
; Sequence 452, Application US/09918585A  
; Publication No. US20030060406A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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CURRENT FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/080105  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-30  
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PRIOR APPLICATION NUMBER: 60/084414  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086023

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYKPEKQEMTWASAEKFCSEQAKGHLISVETALASFPDNLVLA-N 60  
DB 38 ISCPKSKAYGSPYALFLSPKSMMDADLAC-QKRPCKLVSYLSGAEKGSFVSLVSIS 96  
QY 61 KEVLTYIWIQGLVQNKQGPCSSISYE-----NVDPECFMVASDTR 103  
DB 97 NSY--STIWGLDPTQSGSPDDGDGWEWSSTDVNNYFAWEKNDSTIINPHGCSLSKSTG 154  
QY 104 LREMPKVDCEQHSFICKF 122  
DB 155 FLKMKDYNCDAKLPYVCKF 173

RESULT 46  
US-09-999-834A-452  
; Sequence 452, Application US/09999834A  
; Publication No. US20030064407A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C75  
CURRENT APPLICATION NUMBER: US/09/999,834A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LECPSGWSSTDRYCKPPEKQENTMASERFCSQAKGHLISVETALASFPDNLVA-N 60  
DB 38 ISCPGSAVAYGSPCALPLSPKSWMDADLAC-QKRPSSKLTVSLVGAGSFVSLVRIS 96  
QY 61 KEYLTRYIWMIGLRYONKQOPCSSISYE-----NLVDPFCFMVSRPTR 103  
DB 97 NSY--SYIWMIGLHDTQSGSEPDGDGMEWSSTDWNYFAMENKPNPSTIILNPGHGSLSRSTG 154  
QY 104 LREWFKVDCEQHSFTCKF 122  
DB 155 FLKWDVNCDAKLPYVCKF 173

RESULT 47  
US-09-978-423A-452  
Sequence 452, Application US/09978423A  
Publication No. US20030069178A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David



APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Hillen, Kenneth J.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C21  
CURRENT APPLICATION NUMBER: US/09/978,423A  
CURRENT FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
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PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LBCPSGWSSTDRYCYKPFKQEMTWASAEFCEQAKGHLSEVTALASFPDVLVYA-N 60  
DB 38 ISCPGSKAYGSPCTALFLSPKSMWDADLAC-QKRPSSGLTVVLSCAGBSFVSSLVRSIS 96  
QY 61 KYLYRYIWTIGLRVQKGGPCSSISYE-----NLVDFECCFWMSRDR 103  
DB 97 NSY--SYIWIIGLHDPQSGSEPDGDGWEWSSTDVNNYFAWEKNPSTILNCGHSGISRSRG 154  
QY 104 LREWFVDEQGHSPICKF 122  
DB 155 FLKMDYNDCAKLPYVCKF 173

RESULT 48  
US-09-978-193A-452  
Sequence 452, Application US/09978193A  
Publication No. US2003073624A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC6  
CURRENT APPLICATION NUMBER: US/09/978,193A  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;  
Qy 2 LECPSGMSSTDRRCYCFKQEMTWASAEFCSBOAKGCHLTSVETALASFDVNTVYA-N 60  
Db 38 ISCPKSKAYGSCYVLFSPKSMKADLAC-QKRSGLTVSVLSGAEFSFVSLVRSIS 96  
Qy 61 KEYLTRYIWIQLRVONKQGPCSSISYE-----NLVDPCECFMVSROTR 103  
Db 97 NSY--SYIWIQLHDPQSGSEPDGDGWMGMSSTVMNYFAWEKPNSTILNPGHCGSLSRSTG 154  
Qy 104 LREWFVDEQCHSFICKF 122  
Db 155 FLKMKDYNCDAKLPYCKF 173

RESULT 49  
US-09-999-830A-452  
; Sequence 452, Application US/09999830A  
; Publication No. US2003007700A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

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APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C70  
CURRENT APPLICATION NUMBER: US/09/999,830A  
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Query Match 21.4%; Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

QY 2 LECPSGWSSTRDYCYKPEKQEMTWASAEPCSOAKGHLSTVETALASVFNVLVA-N 60  
DB 38 ISCPKSKAAGSCFYALFLSPKSMDDDLAC-QKRPBGKLVSVLSGAGSFVSLVSI 96  
QY 61 KEYLTLYIWIGLAVQNKQPCSSISYE-----NIVDPEECFVMSRDT 103  
DB 97 NSY--SYIWIGLHDPQGSBPDGDGWEWSSTDVNNYFAWEKNPSTILNPGHCSLSRSTG 154  
QY 104 LREMFVDEGQGHSTCKF 122  
DB 155 FLKWKDYNCDAKLPYCKF 173

RESULT 50  
US-09-978-757A-452  
; Sequence 452, Application US/09978757A  
; Publication No. US20030083248A1  
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCES: P2630P1C26  
;; CURRENT APPLICATION NUMBER: US/09/978,757A  
;; CURRENT FILING DATE: 2002-03-19  
;; PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4% Score 148.5; DB 10; Length 175;  
Best Local Similarity 25.9%; Pred. No. 8e-09; Mismatches 57; Indels 21; Gaps 4;  
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;  
QY 2 LECPSGWSSTDRYCYKPPKQEWMTASAEFCSQAKGSHLSVETALPASFVDNLVA-N 60  
DB 38 ISCPKGSKAYGSPCALFLSPKSMWMDADLAC-QKRPSSKLVSVLSGAGSFSVSLVRIS 96  
QY 61 KEYLTRYIWIIGLRVONKQPCSSISYE-----NLVDFECFMVSRDTR 103  
DB 97 NSY--SYIWIIGLHPTQSEPDGDEWGSTVDVNNYFAMEKNPSTIILNPGHGSLSRSTG 154  
QY 104 LREWFKVDCEQHSIFCKF 122  
DB 155 FLKWKDYNCDAKLPYVCKF 173

Search completed: May 2, 2005, 16:07:34  
Job time : 58 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:07 / Search time 24 Seconds  
(without alignments)  
391.908 Million cell updates/sec

Title: US-10-749-387-1

Perfect score: 695  
Sequence: 1 DLECPGMSSTDRYCYKPFK.....MFKVDCQHSFICKFTPR 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 65 summaries

Database :

Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	695	100.0	126	4	US-09-969-763-1 Sequence 1, Appl1
2	684	98.4	126	2	US-08-612-840A-2 Sequence 2, Appl1
3	684	98.4	149	2	US-08-612-840A-8 Sequence 8, Appl1
4	684	98.4	149	4	US-09-969-763-3 Sequence 3, Appl1
5	661	95.1	127	1	US-07-614-443A-1 Sequence 1, Appl1
6	661	95.1	127	1	US-08-294-859-1 Sequence 1, Appl1
7	661	95.1	127	1	US-08-481-676-1 Sequence 1, Appl1
8	661	95.1	127	1	US-09-969-763-10 Sequence 10, Appl1
9	340.5	49.0	130	5	PCT-US92-10344-7 Sequence 7, Appl1
10	340.5	49.0	130	5	PCT-US92-10344-7 Sequence 7, Appl1
11	326.5	47.0	131	1	US-07-893-929A-1 Sequence 1, Appl1
12	326.5	47.0	131	1	PCT-US92-10344-1 Sequence 1, Appl1
13	325.5	46.8	132	1	US-07-893-929A-5 Sequence 5, Appl1
14	325.5	46.8	132	5	PCT-US92-10344-5 Sequence 5, Appl1
15	307.5	44.2	134	5	US-07-893-929A-2 Sequence 2, Appl1
16	307.5	44.2	134	5	PCT-US92-10344-2 Sequence 2, Appl1
17	271.5	39.1	129	4	US-09-058-740-2 Sequence 2, Appl1
18	256.5	36.9	133	1	US-07-893-929A-9 Sequence 9, Appl1
19	256.5	36.9	133	5	PCT-US92-10344-9 Sequence 9, Appl1
20	251.5	36.2	123	5	US-07-893-929A-4 Sequence 4, Appl1
21	251.5	36.2	123	5	PCT-US92-10344-4 Sequence 4, Appl1
22	211.5	30.4	117	1	US-07-614-443A-2 Sequence 2, Appl1
23	211.5	30.4	117	1	US-08-294-859-2 Sequence 2, Appl1
24	211.5	30.4	117	1	US-08-481-676-2 Sequence 2, Appl1
25	208	29.9	38	2	US-08-612-840A-1 Sequence 1, Appl1
26	200	28.8	107	1	US-07-893-929A-6 Sequence 6, Appl1
27	200	28.8	107	5	PCT-US92-10344-6 Sequence 6, Appl1

## ALIGNMENTS

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29	188.5	27.1	125	5	PCT-US92-10344-3 Sequence 3, Appl1
30	168	24.2	144	4	US-09-949-016-10685 Sequence 10685, A
31	168	24.2	166	4	US-09-949-016-6286 Sequence 6286, Ap
32	164	23.6	50	1	US-07-614-443A-5 Sequence 5, Appl1
33	164	23.6	50	1	US-08-294-859-5 Sequence 5, Appl1
34	164	23.6	50	1	US-08-481-676-5 Sequence 5, Appl1
35	162.5	23.4	175	2	US-08-401-530A-3 Sequence 3, Appl1
36	162.5	23.4	175	2	US-08-709-662-3 Sequence 3, Appl1
37	158	22.7	123	1	US-07-893-929A-10 Sequence 10, Appl1
38	158	22.7	123	5	PCT-US92-10344-10 Sequence 10, Appl1
39	153.5	22.1	175	2	US-08-464-637-2 Sequence 2, Appl1
40	153.5	22.1	175	2	US-08-401-530A-4 Sequence 4, Appl1
41	153.5	22.1	175	2	US-08-709-662-4 Sequence 4, Appl1
42	153.5	22.1	175	2	US-08-822-261-3 Sequence 3, Appl1
43	153.5	22.1	175	4	US-09-226-852-3 Sequence 3, Appl1
44	153.5	22.1	183	4	US-09-949-016-10537 Sequence 10537, A
45	151	21.7	165	2	US-08-401-530A-7 Sequence 7, Appl1
46	151	21.7	165	2	US-08-729-103-3 Sequence 3, Appl1
47	151	21.7	165	2	US-08-709-662-7 Sequence 7, Appl1
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49	148.5	21.4	128	5	PCT-US92-10344-8 Sequence 8, Appl1
50	148.5	21.4	175	2	US-08-822-261-1 Sequence 1, Appl1
51	148.5	21.4	175	4	US-09-226-852-1 Sequence 1, Appl1
52	147	21.2	166	2	US-08-729-103-4 Sequence 4, Appl1
53	147	21.2	174	4	US-09-949-016-10686 Sequence 10686, A
54	143.5	20.6	158	2	US-08-729-103-1 Sequence 1, Appl1
55	143.5	20.6	158	2	US-08-468-413-2 Sequence 2, Appl1
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57	143.5	20.6	158	5	PCT-US95-07169-2 Sequence 2, Appl1
58	143.5	20.6	912	5	PCT-US95-03747-2 Sequence 7, Appl1
59	142.5	20.5	174	1	US-07-778-156-7 Sequence 7, Appl1
60	142.5	20.5	174	2	US-08-822-261-4 Sequence 4, Appl1
61	142.5	20.5	174	2	US-08-822-166-7 Sequence 7, Appl1
62	142.5	20.5	174	4	US-09-226-852-4 Sequence 4, Appl1
63	142.5	20.5	1663	1	US-08-220-603A-11 Sequence 11, Appl1
64	140.5	20.2	174	2	US-08-401-530A-2 Sequence 2, Appl1
65	140.5	20.2	174	2	US-08-709-662-2 Sequence 2, Appl1

RESULT 1  
US-09-969-763-1  
; Sequence 1, Application US/09969763  
; Patent No. 6710031  
; GENERAL INFORMATION:  
; APPLICANT: FUJUCHI, NAOYUKI  
; APPLICANT: KITO, MORIKAZU  
; APPLICANT: KAYAHARA, TAKASHI  
; APPLICANT: FUJIKI, FUMIE  
; APPLICANT: ISHIKAWA, KOIKI  
; APPLICANT: SUZUKI, EIICHIRO  
; APPLICANT: GONDOH, KEIKO  
; APPLICANT: SHIMBA, NOBUHISA  
; APPLICANT: YAMADA, NAOYUKI  
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH  
; FILE REFERENCE: 214760USO  
; CURRENT APPLICATION NUMBER: US/09/969,763  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: JP 2000-305279  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Crocotalus horridus  
US-09-969-763-1  
Query Match 100.0%; Score 695; DB 4; Length 126;  
Best Local Similarity 100.0%; Pred. No. 7,9e-78;

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QY	61	KEYLTRYTWIGLARVONKGPCSSISTEYALVDPFECFMYSRDTRLRWEFVNDCEQHSFTC	120							
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QY	121	KFTPRR	126							
Db	121	KFTPRR	126							

RESULT 2  
 US-08-612-840A-2  
 / Sequence 2, Application US/08612840A  
 / Patent No. 5856126  
 / GENERAL INFORMATION:  
 / APPLICANT: FUKUCHI, Naoyuki  
 / APPLICANT: YAMAMOTO, Hiroshi  
 / APPLICANT: NAGANO, Mitsuyo  
 / APPLICANT: KITO, Morikazu  
 / APPLICANT: TANAKA, Akiko  
 / APPLICANT: ISHII, Koichi  
 / APPLICANT: KOBAYASHI, Tsuyoshi  
 / APPLICANT: YOSHIMOTO, Ryota  
 / TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND  
 / TITLE OF INVENTION: METHOD OF PRODUCING THE SAME  
 / NUMBER OF SEQUENCES: 15  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Oblon, Spivak, McJeliland, Maier & Neustadt, P.C.  
 / STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 / City: Arlington  
 / STATE: VA  
 / COUNTRY: USA  
 / ZIP: 22202  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: FastSeq Version 1.5  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/612,840A  
 / FILING DATE: 20-MAR-1996  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: JP 5-236975  
 / FILING DATE: 22-SEP-1993  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: No. 5856126man F. Oblon  
 / REGISTRATION NUMBER: 24,618  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 703-413-3000  
 / TELEFAX: 703-413-2220  
 / INFORMATION FOR SEQ ID NO: 2:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 126 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: peptide  
 / US-08-612-840A-2

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Best Local Similarity	98.4%	Pred. No. 1.8e-76		
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Db	1	DLECSGMSSTDRYCYKPFKQEMTNADARFCSEQAKGCHLLSVFPALEASFPDNTLYAN	60	
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Db 61 KEYLTYIIGLRVONKQPCSSISTENLVDPFECFVNSRPTRLREMFXYDCBQNSH FIC 120  
 QY 121 KFTTRR 126  
 Db 121 KFTTRR 126

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1      RESULT 3
2      US-08-612-840A-8
3      Sequence 8, Application US/08612840A
4      Patent No. 5856126
5      GENERAL INFORMATION:
6      APPLICANT: FUKUCHI, Naoyuki
7      APPLICANT: YAMAMOTO, Hiroshi
8      APPLICANT: NAGANO, Mitsuyo
9      APPLICANT: KITO, Morikazu
10     APPLICANT: TANAKA, Akiko
11     APPLICANT: ISHII, Koichi
12     APPLICANT: KOBAYASHI, Tsuyoshi
13     APPLICANT: YOSHIMOTO, Ryota
14     TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
15     TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
16     NUMBER OF SEQUENCES: 15
17     CORRESPONDENCE ADDRESS:
18     ADDRESSEE: Obton, Spivak, McClelland, Maier & Neustadt, P.C.
19     STREET: 1755 S. Jefferson Davis Highway, Suite 400
20     CITY: Arlington
21     STATE: VA
22     COUNTRY: USA
23     ZIP: 22202
24     COMPUTER READABLE FORM:
25     MEDIUM TYPE: Floppy disk
26     COMPUTER: IBM PC compatible
27     OPERATING SYSTEM: PC-DOS/MS-DOS
28     SOFTWARE: FastSEO Version 1.5
29     CURRENT APPLICATION DATA:
30     APPLICATION NUMBER: US/08/612,840A
31     FILING DATE: 20-MAR-1996
32     CLASSIFICATION: 435
33     PRIOR APPLICATION DATA:
34     APPLICATION NUMBER: JP 5-236975
35     FILING DATE: 22-SEP-1993
36     ATTORNEY/AGENT INFORMATION:
37     NAME: No. 5856126man F. Obton
38     REGISTRATION NUMBER: 24,618
39     TELECOMMUNICATION INFORMATION:
40     TELEPHONE: 703-413-3000
41     TELEFAX: 703-413-2220
42     INFORMATION FOR SEQ ID NO: 8:
43     SEQUENCE CHARACTERISTICS:
44     LENGTH: 149 amino acids
45     TYPE: amino acid
46     TOPOLOGY: linear
47     MOLECULE TYPE: peptide
48     US-08-612-840A-8

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Query Match Similarity	98.4%	Score 684	DB 2	Length 149
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Db	24	DLECPGMSSTDRCYKPFKQEMTWADAEKFCSEQAKGHLISVETALEASFDVNVLYAN	83	
Qy	61	KYLLTRYYTWIGLRVONKQPCSSISYEUNLDPFEECFMYSRDRRLREWEKVCQEQHSFIC	120	
Db	84	KYLLTRYYTWIGLRVONKQPCSSISYEUNLDPFEECFMYSRDRRLREWEKVCDEQEQHSFIC	143	
Qy	121	KFTRRP	126	
Db	144	KFTRRP	149	



RESULT 4  
US-09-969-763-3  
; Sequence 3, Application US/09969763  
; Patent No. 6710031  
; GENERAL INFORMATION:  
; APPLICANT: FUKUCHI, NAOYUKI  
; APPLICANT: KITO, MORIKAZU  
; APPLICANT: KAWAHARA, TAKASHI  
; APPLICANT: FUTAKI, FUMIE  
; APPLICANT: ISHIKAWA, KOIKI  
; APPLICANT: SUZUKI, EIICHIRO  
; APPLICANT: GONDOH, KEIKO  
; APPLICANT: SHIMBA, NOBUHISA  
; APPLICANT: YAMADA, NAOYUKI  
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT  
; FILE REFERENCE: 214760US0  
; CURRENT APPLICATION NUMBER: US/09/969, 763  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: JP 2000-305279  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Crocotalus harridus  
US-09-969-763-3

Query Match 98.4%; Score 684; DB 4; Length 149;  
Best Local Similarity 98.4%; Pred. No. 2, 2e-76;  
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 24 DIECPGMSSTDYCYKPKFQEMTWADAEFCSEQAKGHLISVETALASFDVNTLYAN 83  
QY 61 KEYLTYIWIIGLRVQNKQPCSSISENTLVDPCECFMVSRTLRLEWFKVDCQOHSFIC 120  
DB 84 KEYLTYIWIIGLRVQNKQPCSSISENTLVDPCECFMVSRTLRLEWFKVDCQOHSFIC 143  
QY 121 KFTRRP 126  
DB 144 KFTRRP 149

RESULT 5  
US-07-614-443A-1  
; Sequence 1, Application US/07614443A  
; Patent No. 5342830  
; GENERAL INFORMATION:  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/614,443A  
; FILING DATE: 19901116  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 22803-20003.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-614-443A-1

Query Match 95.1%; Score 661; DB 1; Length 127;  
Best Local Similarity 96.0%; Pred. No. 1, 2e-73;  
Matches 121; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1 DIECPGMSSTDYCYKPKFQEMTWADAEFCSEQAKGHLISVETALASFDVNTLYAN 60  
QY 61 KEYLTYIWIIGLRVQNKQPCSSISENTLVDPCECFMVSRTLRLEWFKVDCQOHSFIC 120  
DB 61 KEYLTYIWIIGLRVQNKQPCSSISENTLVDPCECFMVSRTLRLEWFKVDCQOHSFIC 120  
QY 121 KFTRRP 126  
DB 121 KFTRRP 126

RESULT 6  
US-08-294-859-1  
; Sequence 1, Application US/08294859  
; Patent No. 5679542  
; GENERAL INFORMATION:  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/294, 859  
; FILING DATE: 29-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2803-0003.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-294-859-1

Query Match 95.1%; Score 661; DB 1; Length 127;  
Best Local Similarity 96.0%; Pred. No. 1, 2e-73;  
Matches 121; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	DIECPGWSSTDRYCYKPKPKOEMTASASERPCSEQAKGHLISYETALIEAFVNDNVIYAN	60
Db	1	DIECPGWSSTDRYCYKPKPKOEMTADARPCSEQAKRHLSIYETALIEAFVNDNVIYAN	60
Qy	61	KEVLTIRYIMIGLRVQNKGPCCSIISYENLVDPFECFMYSRDTRLREMKVYDCQOHSFIC	120
Db	61	KEVLTIRYIMIGLRVQNKGPCCSIISYENLVDPFECFMYSRDTRLREMKVYDCQOHSFIC	120
Qy	121	KFTTRPR	126
Db	121	KFTTRPR	126

## RESULT 7

US-08-481-676-1  
Sequence 1, Application US/08481676  
Patent No. 5744584  
GENERAL INFORMATION:  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
City: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,676  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/294,859  
FILING DATE: 29-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2803-0003.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Query Match	95.1%	Score 661	DB 1	Length 127
Best Local Similarity	96.0%	Pred. No. 1.2e-73		
Matches 121; Conservative	0	Mismatches 5	Indels 0	Gaps 0

QY	1	DLPEPSMSSSDRYCYPFQEOETMASARFCEQOKGSHLTSTALAEAFVNVIYAN	60
Db	1	DLPEPSMSSSDRYCYKPFQEMTWADAEKFCSEQAKGSHLTSTALAEAFVNVIYAN	60
QY	61	KEYLTRITWIGLIVONKQPCSSISYENIVDPCEPMYSRDLRLAEKFWVCEQOHSFIC	120
Db	61	KEYLTRITWIGLIVONKQPCSSISYENIVDPCEPMYSRDLRLAEKFWVCEQOHSFIC	120
QY	121	KETRPRL	126
Db	121	KETRPRL	126

## RESULT 8

```

US-09-969-763-10
: Sequence 10, Application US/09969763
: Patent No. 6710631
: GENERAL INFORMATION:
: APPLICANT: FUKUCHI, NAOYUKI
: APPLICANT: KIYO, MORIYASU
: APPLICANT: KAWAHARA, TAKASHI
: APPLICANT: FUTAKI, FUMIE
: APPLICANT: ISHIKAWA, KOIKI
: APPLICANT: SUZUKI, EIICHIRO
: APPLICANT: GONOH, KEIKO
: APPLICANT: SHIMBA, NOBUHISA
: APPLICANT: YAMADA, NAOYUKI
: TITLE OF INVENTION: PROTEIN HAVING ANTITHT
: FILE REFERENCE: 2147600S0
: CURRENT APPLICATION NUMBER: US/09/969,763
: CURRENT FILING DATE: 2000-10-25
: PRIOR APPLICATION NUMBER: JP 2000-305279
: PRIOR FILING DATE: 2000-10-04
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 110
: TYPE: PRT
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-969-763-10

```

Query Match 78.0%; Score 542; DB 4; Length 110;

Best Local Similarity 81.7%; Pred.No. 4.8e-59;  
Matches 103; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

```

Oy 1 DLPCPGMSSTORYCYKPKFQKEMTWASERFCSBQAKGHLSTYETLHESFVDNVLYAN 60
Db 1 DLCPBGMSSYSYCYKPKFQKEMTYADARFCSBQAKGHLSTYETLHESFVDNVLYAN 60
Oy 61 KEVLTBYIWIGLAVQNKGPCCSSISYENLVDPFECFVMSRDLRLREWFKYDCQOHSFIC 120
Db 61 KEVLTIRIWIGLNFFF-----FECFVMSRDLRLREWFKYDCQOHSFIC 104
Oy 121 KFTTRPR 126
Db 105 KFTTRPR 110

```

## RESULT 9

US-07-893-929A-7  
Sequence 7, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Abdoagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common  
ADDRESSER: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893, 929A  
FILING DATE: 19920605

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 533667e  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-7

Query Match  
Best Local Similarity 49.0%; Score 340.5; DB 1; Length 130;  
Matches 66; Conservative 22; Mismatches 29; Indels 13; Gaps 4;

QY 3 ECPGWSSTDRYCYKPFKQEMTWSAERFCSQAKGHLISVETALASFDVNLVAN-K 61  
DB 1 DCPDMSFQYCYQIVKELKTWEDARFCSEQANDGHLVSIRESYEAFAVALLSENYK 60  
QY 62 EYLRITWIGLRVQNGQPC-----SSISTENLV--DPFECFMSRDTRLREMKVDC 112  
DB 61 KY--HWIIGLSVQNGQCSSEWSDGSSVSYENLVKPNKCFVLKKESEFTWMSNYC 117  
QY 113 EOGHSFICK 122  
DB 118 EOGHIFMCKF 127

RESULT 10  
PCT-US92-10344-7  
Sequence 7, Application PC/TUS9210344  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Temple University - Of The Common-  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549

TELEX: None  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-7

Query Match  
Best Local Similarity 49.0%; Score 340.5; DB 5; Length 130;  
Matches 66; Conservative 22; Mismatches 29; Indels 13; Gaps 4;

QY 3 ECPGWSSTDRYCYKPFKQEMTWSAERFCSQAKGHLISVETALASFDVNLVAN-K 61  
DB 1 DCPDMSFQYCYQIVKELKTWEDARFCSEQANDGHLVSIRESYEAFAVALLSENYK 60  
QY 62 EYLRITWIGLRVQNGQPC-----SSISTENLV--DPFECFMSRDTRLREMKVDC 112  
DB 61 KY--HWIIGLSVQNGQCSSEWSDGSSVSYENLVKPNKCFVLKKESEFTWMSNYC 117  
QY 113 EOGHSFICK 122  
DB 118 EOGHIFMCKF 127

RESULT 11  
US-07-893-929A-1  
Sequence 1, Application US/07893929A  
Patent No. 533667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Temple University - Of The Common-  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893, 929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 533667e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-1

Query Match  
Best Local Similarity 47.0%; Score 326.5; DB 1; Length 131;  
Matches 66; Conservative 22; Mismatches 29; Indels 13; Gaps 4;

[illegible][illegible]

Db 121 HEYFVCKEXR 131

RESULT 13  
 US-07-893-929A-5  
 : Sequence 5, Application US/07893929A  
 : Patent No. 533667  
 : GENERAL INFORMATION:  
 : APPLICANT: Kirby, Edward P.  
 : APPLICANT: Peng, Man-ling  
 : TITLE OF INVENTION: Alboaggregins: Platelet  
 : TITLE OF INVENTION: Agonists Which Bind To Platelet  
 : TITLE OF INVENTION: Membrane Glycoprotein Ib  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Temple University - Of The Common-  
 : ADDRESS: Health System of Higher Education  
 : STREET: 406 University Services Building  
 : CITY: Philadelphia  
 : STATE: Pennsylvania  
 : COUNTRY: U.S.A.  
 : ZIP: 19122  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
 : COMPUTER: IBM PS/2  
 : OPERATING SYSTEM: MS-DOS  
 : SOFTWARE: Wordperfect 5.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/07/893, 929A  
 : FILING DATE: 19920605  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/803, 630  
 : FILING DATE: December 3, 1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Monaco, Daniel A.  
 : REGISTRATION NUMBER: 30,480  
 : REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (215) 568-8383  
 : TELEFAX: (215) 568-5549  
 : TELEX: NO. 5336667e  
 : INFORMATION FOR SEQ ID NO: 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 132 amino acids  
 : TYPE: AMINO ACID  
 : TOPOLOGY: linear  
 : US-07-893-929A-5

```

Query Match      46.8%  Score 325.5; DB 1; Length 132;
Best Local Similarity 47.3%  Pred. No. 3e-32;
Matches          61;  Conservative 22;  Mismatches 37;  Indels 9;  Gaps 2;

QY      3  ECPGWSMTDRDYCKPFEKQEMTWASAEKFCSEQAKGHLSVETALKEASFPVDNLYANKE 62
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1  DCPSPMSFKQYCYQIVKELTKWEDAEKFCSEQANDGHLVISEYREAVFAELLSENVK 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      63  YLTRYIWIIGLVONKQKPC-----SSISYENLV--DPEFCFVMSRDTLRLEMPKDC 113
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      61  TTKYVWVWIGLSVONKEQCCSEMSDGSXVYENLILKPPKRCFVLKKESEFRRTSNVYCE 120
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      114  QOHSFICKF 122
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB      121  QKHIFMCKF 129
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

RESULT 14
PCT-US92-10344-5
; Sequence 5, Application PC/TUS9210344
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-jing

```



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-2

Query Match 44.2%; Score 307.5; DB 5; Length 134;  
Best Local Similarity 42.0%; Pred. No. 5.1e-30;  
Matches 55; Conservative 26; Mismatches 41; Indels 9; Gaps 2;

QY 1 DLEPGMSSTDRYCYKPFQKQEMTWSAERFCSQAKGHLISVETALIASFVDNVLANK 60  
DB 1 DFLCLPGMSAYDYCYKRVFNEPKWEDAEKQADSGHLVSIETMGADFAVLAOLISEN 60  
QY 61 KEVLTYYWIGLAVONKQGPC-----SSISYENLVDPF--ECFVMSRDLRLREWEKVD 111  
DB 61 IQSKEHYWIGLAVONKQGCSSMSDSSVTEIENIKYKRCGLAEQSGRKINING 120  
QY 112 CEQSHSFICKF 122  
DB 121 CIQLNPFVCKF 131

RESULT 17  
US-09-058-740-2  
Sequence 2, Application US/09058740  
Patent No. 6489451  
GENERAL INFORMATION:

APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,  
Jing Liu, Li-Wen Niu, Wan-Zhi Huang,  
Zhen-Yu Xu, Dan Luo, Lian-Di Kang,  
Jin-Guo Ding, Fang Rong, Yan Liu and  
Hui-Ran Chen  
TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE  
VENOM OF AGKISTROON ACUTUS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/058,740  
FILING DATE: 10-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chen, Anthony C.  
REGISTRATION NUMBER: 38,673  
REFERENCE/DOCKET NUMBER: 233/298

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-058-740-2

Query Match 39.1%; Score 271.5; DB 4; Length 129;  
Best Local Similarity 41.4%; Pred. No. 1.3e-25;  
Matches 53; Conservative 22; Mismatches 44; Indels 9; Gaps 2;

QY 3 ECPGMSSTDRYCYKPFQKQEMTWSAERFCSQAKGHLISVETALIASFVDNVLANK 62  
DB 1 DCSMSVYEGHCYKVFQSKTWTDAESFCTKQVNGHLVSISSGEADFVGLIAQKIX 60  
QY 63 YLTRYIWLGRVONKGPC-----SSISYENLV--DFECFVMSRDLRLREWEKVD 113  
DB 61 SAKIHWIGLRAQNKQCSISMSDSSISKENWIEESKCLGVHIEFGHKWENFYCE 120  
QY 114 QQSHFICK 121  
DB 121 QDDPFVCE 128

RESULT 18  
US-07-893-929A-9  
Sequence 9, Application US/07893929A  
Patent No. 5336657  
GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893,929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5336667e  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-9

Query Match 36.9%; Score 256.5; DB 1; Length 133;

Best Local Similarity 37.8%; Pred. No. 9.8e-24;  
Matches 51; Conservative 30; Mismatches 43; Indels 11; Gaps 4;

QY 1 DLECPGMSSTDRYCYKFKQEMTWASAEKFCSEQAKGHLISVETALASFPVDNVLVAN 60

DB 1 DDCLSGMSYEGHCTQLFRK-TWDEAKYCN-QMDGHLVIESNAKAFVAQLISRK 58

QY 61 --KEYLTRYIWIIGLRYONKQPC-----SSISYENLVDPFECFVNSRDTLRREPKVD 111

DB 59 LPKSAIEDRWYIGLRRSKREOCGHLMTDNTSPFVHYEHVPTKCFVLERQTERFKMIVAN 118

QY 112 CEQSHFICKFTRPR 126

DB 119 CEFKPFVCKAKIPR 133

## RESULT 19

PCT-US92-10344-9  
Sequence 9, Application PC/TUS9210344

GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.

APPLICANT: Peng, Man-ling

TITLE OF INVENTION: Alboagregins: Platelet

TITLE OF INVENTION: Agonists Which Bind To Platelet

TITLE OF INVENTION: Membrane Glycoprotein Ib

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of The Common-

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10344

FILING DATE: 19921201

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/803,630

FILING DATE: December 3, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: None

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

PCT-US92-10344-9

Query Match 36.9%; Score 256.5; DB 5; Length 133;

Best Local Similarity 37.8%; Pred. No. 9.8e-24;  
Matches 51; Conservative 30; Mismatches 43; Indels 11; Gaps 4;

QY 1 DLECPGMSSTDRYCYKFKQEMTWASAEKFCSEQAKGHLISVETALASFPVDNVLVAN 60

DB 1 DDCLSGMSYEGHCTQLFRK-TWDEAKYCN-QMDGHLVIESNAKAFVAQLISRK 58

QY 61 --KEYLTRYIWIIGLRYONKQPC-----SSISYENLVDPFECFVNSRDTLRREPKVD 111

DB 59 LPKSAIEDRWYIGLRRSKREOCGHLMTDNTSPFVHYEHVPTKCFVLERQTERFKMIVAN 118

QY 112 CEQSHFICKFTRPR 126

DB 119 CEFKPFVCKAKIPR 133

## RESULT 20

US-07-893-929A-4  
Sequence 4, Application US/07893929A

Patent No. 5336667

GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.

APPLICANT: Peng, Man-ling

TITLE OF INVENTION: Alboagregins: Platelet

TITLE OF INVENTION: Agonists Which Bind To Platelet

TITLE OF INVENTION: Membrane Glycoprotein Ib

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of The Common-

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/893,929A

FILING DATE: 19920605

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/803,630

FILING DATE: December 3, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5336667e

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-893-929A-4

Query Match 36.2%; Score 251.5; DB 1; Length 123;

Best Local Similarity 39.7%; Pred. No. 3.7e-23;  
Matches 52; Conservative 22; Mismatches 36; Indels 21; Gaps 6;

QY 3 ECPGMSSTDRYCYKFKQEMTWASAEKFCSEQAKGHLISVETALASFPVDN----VLV 58

DB 1 DCPGMSSTDRYCYKFKQEMTWASAEKFCSEQAKGHLISVETALASFPVDN----VLV 60

QY 59 ANKEYLTRYIWIIGLRYONKQPCSS-----ISYENLVDPFECFVNSRDTLRREPKVD 111

DB 61 AN-----LVWIGL--SNLMGNSQMSDGTLDYCKWREQFEC-LVSRITN-NEWLSMD 110

QY 112 CEQSHFICKF 122

DB 111 CSSTHSFVCEP 121

RESULT 21  
PCT-US92-10344-4  
Sequence 4, Application PC/TUS9210344  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind to Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSEE: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-4

Query Match 36.2%; Score 251.5; DB 5; length 123;  
Best Local Similarity 39.7%; Pred. No. 3.7e-23;  
Matches 52; Conservative 22; Mismatches 36; Indels 21; Gaps 6;

QY 3 ECPGSGSTDRYCYKPFQEMTWASAEFCSEQAKGHLISYETALIASFVFN---VLY 58  
DB 1 DCPSPMSSYEGHCYRFVFNQWADAEKFCCTQOHGKSHLVSFQSSBEADFFVQWTRPILN 60  
QY 59 ANKEYLIRIYIGLRQNGQPCSS-----ISYENLVDPFECFVWSRDTLRWFVKVD 111  
DB 61 AN-----LWVIGL--SNLMGNCNSQWSDGYLDYKXWREQEC-LVSRFTN-NEMLSD 110

QY 112 CEOGHSFICKF 122  
DB 111 GSGTHSFVCEF 121

RESULT 22  
US-07-614-443A-2  
Sequence 2, Application US/07614443A  
Patent No. 5342830  
GENERAL INFORMATION:  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road

CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/614,443A  
FILING DATE: 19901116  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22803-20003.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-614-443A-2

Query Match 30.4%; Score 211.5; DB 1; length 117;  
Best Local Similarity 36.9%; Pred. No. 2.9e-18;  
Matches 45; Conservative 28; Mismatches 42; Indels 7; Gaps 5;

QY 3 ECPGSGSTDRYCYKPFQEMTWASAEFCSEQAKGHLISYETALIASFVFN---VLY 58  
DB 1 DCPSPMSSYEGHCYRFVFNQWADAEKFCCTQOHGKSHLVSFQSSBEADFFVQWTRPILN 60  
QY 63 YL-TRYIWLGRVQ--NKQPCSSISYENLVDPFECFVWSRDTLRWFVKVCEQOHSFIC 120  
DB 61 WMGWMDINNRRLQWSDG---TKVNYKMSAEPCC-IYCRATD-NQWLSTGCKSHNVVC 115

QY 121 KF 122  
DB 116 KF 117

RESULT 23  
US-08-294-859-2  
Sequence 2, Application US/08294859  
Patent No. 5679542  
GENERAL INFORMATION:  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,859  
FILING DATE: 29-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2803-0003.10



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-294-859-2

Query Match 30.4%; Score 211.5; DB 1; Length 117;  
Best Local Similarity 36.9%; Pred. No. 2.9e-18;  
Matches 45; Conservative 28; Mismatches 42; Indels 7; Gaps 5;

QY 3 ECPGSGSSTRDYCYKPKQEMTWASAEFPCSEQAKGHLSTALEASVDVLANKE 62  
DB 1 DCPGSDMSYEGHCYRFFQOEMTWDAEKCTQOHTGHLVSFRSSSEVDPLVSLKFDLP 60  
QY 63 YL-TRYIWIGLRVQ-NKGQPCSSISYENLVDPCECFMVSBDTFLREWFKVDCEQOHSFIC 120  
DB 61 WMGMRIDIMBERRLQWSDG---TKVNYKAMSABPEC-IVCRATD-NQWLSTSCSKTHNVVC 115  
QY 121 KF 122  
DB 116 KF 117

RESULT 24

US-08-481-676-2

Sequence 2, Application US/08481676  
Patent No. 5744584

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS  
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
CITY: Washington, D.C.  
COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,676

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/294,859

FILING DATE: 29-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2803-0003.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-481-676-2

Query Match 30.4%; Score 211.5; DB 1; Length 117;  
Best Local Similarity 36.9%; Pred. No. 2.9e-18;

Matches 45; Conservative 28; Mismatches 42; Indels 7; Gaps 5;

QY 3 ECPGSGSSTRDYCYKPKQEMTWASAEFPCSEQAKGHLSTALEASVDVLANKE 62  
DB 1 DCPGSDMSYEGHCYRFFQOEMTWDAEKCTQOHTGHLVSFRSSSEVDPLVSLKFDLP 60  
QY 63 YL-TRYIWIGLRVQ-NKGQPCSSISYENLVDPCECFMVSBDTFLREWFKVDCEQOHSFIC 120  
DB 61 WMGMRIDIMBERRLQWSDG---TKVNYKAMSABPEC-IVCRATD-NQWLSTSCSKTHNVVC 115  
QY 121 KF 122  
DB 116 KF 117

RESULT 25

US-08-612-840A-1

Sequence 1, Application US/08612840A

Patent No. 5856126

GENERAL INFORMATION:

APPLICANT: FUKUCHI, Naoyuki

APPLICANT: YAMAMOTO, Hiroshi

APPLICANT: NAGANO, Mitsuyo

APPLICANT: KITO, Morikazu

APPLICANT: TANAKA, Akiko

APPLICANT: ISHII, Koichi

APPLICANT: KOBAYASHI, Tanyoshi

APPLICANT: YOSHIMOTO, Ryota

TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND

TITLE OF INVENTION: METHOD OF PRODUCING THE SAME

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oblon, Spivak, McClelland, Maier &amp; Neustadt, P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,840A

FILING DATE: 20-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-236975

FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5856126man F. Oblon

REGISTRATION NUMBER: 24,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-612-840A-1

Query Match 29.9%; Score 208; DB 2; Length 38;  
Best Local Similarity 94.7%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLECPGSGSSTRDYCYKPKQEMTWASAEFPCSEQAKG 38  
DB 1 DLECPGSGSSTRDYCYKPKQEMTWADAEFPCSEQAKG 38

RESULT 26  
US-07-893-929A-6  
Sequence 6, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists which bind to platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSER: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893,929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5336667e  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-6

Query Match 28.8%; Score 200; DB 1; Length 107;  
Best Local Similarity 34.6%; Pred. No. 6,8e-17;  
Matches 44; Conservative 18; Mismatches 37; Indels 28; Gaps 5;

QY 3 ECPGSGSSIDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALIASFVDNVIYANKE 62  
DB 1 DCPSPWSSYDLYCYKVFQORNMWEDAEFCROQHTGSHLSPHSEKADPV----- 51  
QY 63 YLTRYIWIGL-----RVQ-NKGQPCSSISYENLVDPFECFVWSRDRRLRMEFKVDCQ 114  
DB 52 -----WIGLTDVWSACRLQWSDG---TELKYNMTASEC--IASKTTDQWMTWSCSK 100  
QY 115 QHSFICK 121  
DB 101 TYPFVCK 107

RESULT 27  
PCT-US92-10344-6  
Sequence 6, Application PC/TUS9210344  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists which bind to platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSER: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-6

Query Match 28.8%; Score 200; DB 5; Length 107;  
Best Local Similarity 34.6%; Pred. No. 6,8e-17;  
Matches 44; Conservative 18; Mismatches 37; Indels 28; Gaps 5;

QY 3 ECPGSGSSIDRYCYKPFKQEMTWASAEFCSQAKGHLISVETALIASFVDNVIYANKE 62  
DB 1 DCPSPWSSYDLYCYKVFQORNMWEDAEFCROQHTGSHLSPHSEKADPV----- 51  
QY 63 YLTRYIWIGL-----RVQ-NKGQPCSSISYENLVDPFECFVWSRDRRLRMEFKVDCQ 114  
DB 52 -----WIGLTDVWSACRLQWSDG---TELKYNMTASEC--IASKTTDQWMTWSCSK 100  
QY 115 QHSFICK 121  
DB 101 TYPFVCK 107

RESULT 28  
US-07-893-929A-3  
Sequence 3, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists which bind to platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSER: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

```
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5336676
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-893-929A-3

Query Match
Best Local Similarity 27.1%; Score 188.5; DB 1; Length 125;
Matches 42; Conservative 22; Mismatches 49; Indels 13; Gaps 5;

QY 4 CPBGMSSTRDYCYKPKQEMTWASAEPCSEQAKGHLISVETALASPVQNVLYANKY 63
DB 4 CPBGMSSTRDYCYKPKQEMTWASAEPCSEQAKGHLISVETALASPVQNVLYANKY 63
QY 64 LRRYVIGLRVQNKQPCSS-----ISYENLVDPFCFMSRDRRLRMEFVDCQOH 116
DB 64 --DFVMMGL--SDIWKECTKEMSDGARLDYKAMSGKSYC-LVSKTTN-NEMLSMDCSRTL 117
QY 117 SPICKP 122
DB 118 YPVCKF 123

RESULT 29
PCT-US92-10344-3
Sequence 3: Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-Ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESS: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US92-10344-3

Query Match
Best Local Similarity 27.1%; Score 188.5; DB 5; Length 125;
Matches 42; Conservative 22; Mismatches 49; Indels 13; Gaps 5;

QY 4 CPBGMSSTRDYCYKPKQEMTWASAEPCSEQAKGHLISVETALASPVQNVLYANKY 63
DB 4 CPBGMSSTRDYCYKPKQEMTWASAEPCSEQAKGHLISVETALASPVQNVLYANKY 63
QY 64 LRRYVIGLRVQNKQPCSS-----ISYENLVDPFCFMSRDRRLRMEFVDCQOH 116
DB 64 --DFVMMGL--SDIWKECTKEMSDGARLDYKAMSGKSYC-LVSKTTN-NEMLSMDCSRTL 117
QY 117 SPICKP 122
DB 118 YPVCKF 123
```

```
RESULT 30
US-09-949-016-10685
Sequence 10685, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10685
LENGTH: 144
TYPE: PRT
ORGANISM: Human
US-09-949-016-10685

Query Match
Best Local Similarity 24.2%; Score 168; DB 4; Length 144;
Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

QY 2 LECPSGMSSTRDYCYKPKQEMTWASAEPCSEQAKGHLISVETALASPVQNVLYANKY 61
DB 12 ISCPBGSTNAIRSYCYFNEDETRWDADLYC-QNMNSGLVSVLTAEAGAFVASLI---K 67
QY 62 EYLTR--YIWIIGLRVQNKQ-----PCSSISYE-----NVDPFCFMSRDRRLRME 107
DB 68 ESGTDDFNWVIGLHPKRRMRHMSGSLVSYKSWGICGAPSSVNPQYCVSLSSSTGFOKM 127
QY 108 FKVDCQOHSPICKP 122
DB 128 KDVPCEDKPSFVCKP 142
```

RESULT 34  
US-08-481-676-5  
; Sequence 5, Application US/08481676  
; Patent No. 5744584  
; GENERAL INFORMATION:  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morisson & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,676  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/294,859  
FILING DATE: 29-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2803-0003.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-481-676-5

Query Match 23.6%; Score 164; DB 1; Length 50;  
Best Local Similarity 54.0%; Pred. No. 6.8e-13;  
Matches 27; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 3 ECSSGMSSTDRYCYKPPKQEMTWSAERFCSEQAKGHLISVETALDASR 52  
DB 1 DCPSDWSHGHCHYKVFNLKXTWEDAEKFCTEQANGHLVSISSKEANR 50

RESULT 35  
US-08-401-530A-3  
Sequence 3, Application US/08401530A  
Patent No. 5834590  
GENERAL INFORMATION:  
APPLICANT: Vinik, Aaron I.  
APPLICANT: Piltenger, Gary L.  
APPLICANT: Rafaeloff, Ronit  
APPLICANT: Rosenberg, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC  
TITLE OF INVENTION: ISLET NEOGENESIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/401,530A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570.48743  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-401-530A-3

Query Match 23.4%; Score 162.5; DB 2; Length 175;  
Best Local Similarity 30.9%; Pred. No. 5.5e-12;  
Matches 43; Conservative 21; Mismatches 56; Indels 19; Gaps 5;

QY 2 LECPSGMSSTDRYCYKPPKQEMTWSAERFCSEQAKGHLISVETALDASR 61  
DB 38 ISCPKSGQAYGSCYVALFQIPQTFPDABLACORRPE-GHLYSVLVAAEASFLASNV-KOT 95  
QY 62 EYLTRYIWIGLARQN-KGQPCSS-----ISYEN-----LYDPFECFVNSDTRL 104  
DB 96 GNSYQYIWIIGLHDPTLIGSEBNGGEMWSNNDIMYVNERNPSTALDRFCGSLSSSGP 155  
QY 105 REWFKVDCQOHSFICKFT 123  
DB 156 LMRDITTCVLPYCKFT 174

RESULT 36  
US-08-709-662-3  
Sequence 3, Application US/08709662  
Patent No. 5840531  
GENERAL INFORMATION:  
APPLICANT: Vinik, Aaron I.  
APPLICANT: Piltenger, Gary L.  
APPLICANT: Rafaeloff, Ronit  
APPLICANT: Rosenberg, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC  
TITLE OF INVENTION: ISLET NEOGENESIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,662  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570.59178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-709-662-3

Query Match 23.4%; Score 162.5; DB 2; Length 175;  
Best Local Similarity 30.9%; Pred. No. 5.5e-12;  
Matches 43; Conservative 21; Mismatches 56; Indels 19; Gaps 5;

QY 2 LCPGWSSTDRYCYKPKQEMTWSAERPCSEQAKGHLISVETALASFDVNLVANK 61  
DB 38 ISCPKSGSQAVGSYCYALFQIPQTFPDAELACQKRP- GHLSVTLNVAEASFLASWV-KQT 95  
QY 62 EVLTRIYIWIGLRVQNKQPC-----SSISYENLVDPFECFVMSRDTLREMFVKVDCQO 115  
DB 96 GMSYQYIWIWGLHDPDTGGEPNGGGMWMSNNDINNYWERNPSTALDRFCGSLSRSSGF 155  
QY 105 REMFKVDCQOHSFICKT 123  
DB 156 LKRWDTTCVYKLPYCKT 174

RESULT 37  
US-07-893-929A-10  
Sequence 10, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893,929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-5549  
TELEFAX: (215) 568-8383  
TELEX: No. 5336667e  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-10

Query Match 22.7%; Score 158; DB 1; Length 123;

Best Local Similarity 28.6%; Pred. No. 1.2e-11;  
Matches 36; Conservative 18; Mismatches 60; Indels 12; Gaps 4;

QY 4 CPBGWSSTDRYCYKPKQEMTWSAERPCSEQAKGHLISVETA-LEASFVDNLVANK 62  
DB 2 CLPDWSVYEGCYKPKFERMNMADAERFCMKQVKGHLVSFRNSKXXXXXXXXXXXXX 61  
QY 63 YLTRIYIWIGLRVQNKQPC-----SSISYENLVDPFECFVMSRDTLREMFVKVDCQO 115  
DB 62 XKMLVWIGL--SDYWRDCYEWMSDAQDLYKANDNERHCF--AAKTTDNQMRKCSGE 117  
QY 116 HSFICK 121  
DB 118 FYFVCK 123

RESULT 38  
PCT-US92-10344-10  
Sequence 10, Application PC/TUS9210344  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboagregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-10

Query Match 22.7%; Score 158; DB 5; Length 123;  
Best Local Similarity 28.6%; Pred. No. 1.2e-11;  
Matches 36; Conservative 18; Mismatches 60; Indels 12; Gaps 4;

QY 4 CPBGWSSTDRYCYKPKQEMTWSAERPCSEQAKGHLISVETA-LEASFVDNLVANK 62  
DB 2 CLPDWSVYEGCYKPKFERMNMADAERFCMKQVKGHLVSFRNSKXXXXXXXXXXXXX 61  
QY 63 YLTRIYIWIGLRVQNKQPC-----SSISYENLVDPFECFVMSRDTLREMFVKVDCQO 115  
DB 62 XKMLVWIGL--SDYWRDCYEWMSDAQDLYKANDNERHCF--AAKTTDNQMRKCSGE 117

QY 116 HSFICK 121  
DB 118 FYEVCK 123

## RESULT 39

US-08-464-637-2  
Sequence 2, Application US/08464637  
Patent No. 5834214  
GENERAL INFORMATION:  
APPLICANT: Iovanna, Juan-Lucio  
APPLICANT: Dagorn, Jean-Charles  
APPLICANT: Keim, Volker  
TITLE OF INVENTION: Detection of Pancreatitis-Associated  
TITLE OF INVENTION: Protein for diagnosis of Cystic Fibrosis or Pancreatic  
TITLE OF INVENTION: Disease (as amended)  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolaich & Birch, LLP  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-3487  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,637  
FILING DATE: 30-AUG-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 2121-107P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-637-2

Query Match 22.1%; Score 153.5; DB 2; Length 175;  
Best Local Similarity 25.7%; Pred. No. 7, 1e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LECPSGMSSTDRYCYXFEKQMTWASAEFCSEQAKGHLISYETALASFDVNLVA-N 60  
DB 38 IRCPKSKAYGSHCYALFLSPKSWTDADLAC-QKPSGNLVSLSGAEGSFVSLVKSIG 96  
QY 61 KEYLTRYIWIIGLAVONKQGPCSSISYE-----NLVDPECFMVSRDTR 103  
DB 97 NSY--SYVWIGLHDPDPTGTEPNBEGWESSDVWNYFAMERNPSTISSPCHCASLSRSTA 154  
QY 104 LREMFKVDEQCHSFICKFT 123  
DB 155 FLRMKDYNCNVRLLPYCKFT 174

RESULT 40  
US-08-401-530A-4  
Sequence 4, Application US/08401530A  
Patent No. 5834590  
GENERAL INFORMATION:  
APPLICANT: Vink, Aaron I.  
APPLICANT: Pittenger, Gary L.

APPLICANT: Rafaeloff, Ronit  
APPLICANT: Rosenberg, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC  
TITLE OF INVENTION: ISLET NEOGENESIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/401,530A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570.48743  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9299  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-401-530A-4

Query Match 22.1%; Score 153.5; DB 2; Length 175;  
Best Local Similarity 25.7%; Pred. No. 7, 1e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LECPSGMSSTDRYCYXFEKQMTWASAEFCSEQAKGHLISYETALASFDVNLVA-N 60  
DB 38 IRCPKSKAYGSHCYALFLSPKSWTDADLAC-QKPSGNLVSLSGAEGSFVSLVKSIG 96  
QY 61 KEYLTRYIWIIGLAVONKQGPCSSISYE-----NLVDPECFMVSRDTR 103  
DB 97 NSY--SYVWIGLHDPDPTGTEPNBEGWESSDVWNYFAMERNPSTISSPCHCASLSRSTA 154  
QY 104 LREMFKVDEQCHSFICKFT 123  
DB 155 FLRMKDYNCNVRLLPYCKFT 174

RESULT 41  
US-08-709-662-4  
Sequence 4, Application US/08709662  
Patent No. 5840531  
GENERAL INFORMATION:  
APPLICANT: Vink, Aaron I.  
APPLICANT: Pittenger, Gary L.  
APPLICANT: Rafaeloff, Ronit  
APPLICANT: Rosenberg, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC  
TITLE OF INVENTION: ISLET NEOGENESIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington

STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,662  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570.59178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-709-662-4

Query Match 22.1%; Score 153.5; DB 2; Length 175;  
Best Local Similarity 25.7%; Pred. No. 7,1e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LECPSGMSSTDYCYKPFKQEMTWASAEFSCBQAKGHLISVETALBAPVDNVLVA-N 60  
DB 38 IRCPKSKAYGSHCVLFLSPKSWTDADLAC-QKPSGNLVSVLSGAGSFFVSLVKSIG 96

QY 61 KEYLTRYITIGLRVQNKQPCSSISYE-----NLVDPFECFVMSRDTR 103  
DB 97 NSY--SYWVIGLHDPQTGTEPNBEGEWSSSDVMNYFAMERNPSTISSPGHCASLSRSTA 154

QY 104 LRFMFVDCQOHSFICKFT 123  
DB 155 FIRMKDYNQNRLLPYCKFT 174

RESULT 42  
US-08-822-261-3  
Sequence 3, Application US/08822261  
Patent No. 5935813  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,261  
FILING DATE: Filed Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0251 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-845-4166  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 262369  
US-08-822-261-3

Query Match 22.1%; Score 153.5; DB 2; Length 175;  
Best Local Similarity 25.7%; Pred. No. 7,1e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LECPSGMSSTDYCYKPFKQEMTWASAEFSCBQAKGHLISVETALBAPVDNVLVA-N 60  
DB 38 IRCPKSKAYGSHCVLFLSPKSWTDADLAC-QKPSGNLVSVLSGAGSFFVSLVKSIG 96

QY 61 KEYLTRYITIGLRVQNKQPCSSISYE-----NLVDPFECFVMSRDTR 103  
DB 97 NSY--SYWVIGLHDPQTGTEPNBEGEWSSSDVMNYFAMERNPSTISSPGHCASLSRSTA 154

QY 104 LRFMFVDCQOHSFICKFT 123  
DB 155 FIRMKDYNQNRLLPYCKFT 174

RESULT 43  
US-09-226-852-3  
Sequence 3, Application US/09226852  
Patent No. 6492499  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/226,852  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,261  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0251 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-845-0555  
TELEFAX: 415-845-4166



INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 262369  
US-09-226-852-3

Query Match 22.1%; Score 153.5; DB 4; Length 175;  
Best Local Similarity 25.7%; Pred. No. 7.1e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYCPKQEMTWASAEKRCSEQAKGHLISVETALASFDVNLVYA-N 60  
DB 38 IRCPKSGSKAYGSHCYALFLSPKSWTDADLAC-QKRPNGNLVSLGAGSGFVSLVKSIG 96  
QY 61 KEYLTRYIWIIGLRVQNKGPCSSISYE-----NIVDPECFMVRDTR 103  
DB 97 NSY--SYVWIGLHDPFGTEPNNGEWMSSSDVMNTFAMERNSTISSRCHCALSRSIA 154  
QY 104 LREMFVDCQEQHSFICKFT 123  
DB 155 FLRMKDYNCNVRLLPYCKFT 174

RESULT 44  
US-09-949-016-10537  
Sequence 10537, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT FILING DATE: 2000-04-14  
PRIOR FILING DATE: 2000-05-17, 755  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10537  
LENGTH: 183  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10537

Query Match 22.1%; Score 153.5; DB 4; Length 183;  
Best Local Similarity 25.7%; Pred. No. 7.5e-11;  
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

QY 2 LBCPSGMSSTDRYCYCPKQEMTWASAEKRCSEQAKGHLISVETALASFDVNLVYA-N 60  
DB 46 IRCPKSGSKAYGSHCYALFLSPKSWTDADLAC-QKRPNGNLVSLGAGSGFVSLVKSIG 104  
QY 61 KEYLTRYIWIIGLRVQNKGPCSSISYE-----NIVDPECFMVRDTR 103  
DB 105 NSY--SYVWIGLHDPFGTEPNNGEWMSSSDVMNTFAMERNSTISSRCHCALSRSIA 162  
QY 104 LREMFVDCQEQHSFICKFT 123  
DB 163 FLRMKDYNCNVRLLPYCKFT 182

RESULT 45  
US-08-401-530A-7  
Sequence 7, Application US/08401530A

Patent No. 5834590  
GENERAL INFORMATION:  
APPLICANT: Vink, Aaron I.  
APPLICANT: Pittenger, Gary L.  
APPLICANT: Rafaeloff, Ronit  
APPLICANT: Rosenbery, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570.48743  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-401-530A-7

Query Match 21.7%; Score 151; DB 2; Length 165;  
Best Local Similarity 29.6%; Pred. No. 1.3e-10;  
Matches 40; Conservative 26; Mismatches 51; Indels 18; Gaps 5;

QY 2 LBCPSGMSSTDRYCYCPKQEMTWASAEKRCSEQAKGHLISVETALASFDVNLVYANK 61  
DB 33 IRCPGSGNAYSYCYFMEHDLSMAADLFC-QNMNSGYLVSLGAGNPLASLI---K 88  
QY 62 EYLT-RYIWIIGLR-VQNKGPCSSIS-----YENLVDPPECFMVRDTR 107  
DB 89 ESGTTANWIGLHDPKNNRRMHWSSGSLFLYKSWDTGYPNNSNRGCVSYNSGKXW 148  
QY 108 FKYVDCQEQHSFICKFT 122  
DB 149 RDNSCDAQLSFVCKF 163

RESULT 46  
US-08-729-103-3  
Sequence 3, Application US/08729103  
Patent No. 5837841  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,103  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0138 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 393209  
US-08-729-103-3

Query Match. 21.7%; Score 151; DB 2; Length 165;  
Best Local Similarity 29.6%; Pred. No. 1.3e-10;  
Matches 40; Conservative 26; Mismatches 51; Indels 18; Gaps 5;

QY 2 LKPCSGMSTDRYCKPFPQEMTWASAEPCSEQAKGHLISVETALASPVDNVLYANK 61  
DB 33 ITCPEGSNNYSYCYFEMEDHLSMAADLFC-QNNNSGYLVSVLSQAEGNFLASLI---K 88  
QY 62 EYLT--RYIWIGLR--VONKGPCCSIS-----YENLVDPCECFMWSRDTLRBW 107  
DB 89 EGGTTAAVNWIGLHDPKNNRMRHWSGSLFLYKSWDTGYPNNSNNGYCVSVNSGYKKW 148  
QY 108 FKVDEQCHSFICKF 122  
DB 149 RDNSCDAQLSFVCKF 163

RESULT 47  
US-08-709-662-7  
Sequence 7, Application US/08709662  
Patent No. 5840531  
GENERAL INFORMATION:  
APPLICANT: Vinik, Aaron I.  
APPLICANT: Piltenger, Gary L.  
APPLICANT: Rafaeleoff, Ronit  
APPLICANT: Rosenberg, Lawrence  
APPLICANT: Duguid, William P.  
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,662  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 00570,59178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-709-662-7

Query Match. 21.7%; Score 151; DB 2; Length 165;  
Best Local Similarity 29.6%; Pred. No. 1.3e-10;  
Matches 40; Conservative 26; Mismatches 51; Indels 18; Gaps 5;

QY 2 LKPCSGMSTDRYCKPFPQEMTWASAEPCSEQAKGHLISVETALASPVDNVLYANK 61  
DB 33 ITCPEGSNNYSYCYFEMEDHLSMAADLFC-QNNNSGYLVSVLSQAEGNFLASLI---K 88  
QY 62 EYLT--RYIWIGLR--VONKGPCCSIS-----YENLVDPCECFMWSRDTLRBW 107  
DB 89 EGGTTAAVNWIGLHDPKNNRMRHWSGSLFLYKSWDTGYPNNSNNGYCVSVNSGYKKW 148  
QY 108 FKVDEQCHSFICKF 122  
DB 149 RDNSCDAQLSFVCKF 163

RESULT 48  
US-07-893-929A-8  
Sequence 8, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
APPLICANT: Peng, Man-ling  
TITLE OF INVENTION: Alboaggregins: Platelet  
TITLE OF INVENTION: Agonists which Bind To Platelet  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: Wealth System Of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893,929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.



Qy 61 KEYLPRYINIGLRVONKQPCSSISYE-----NYDPFEGFMYSPDTR 103  
Db 97 NSY--SYIWIIGLHDPYQSGSEPDGDEWSSTDVMMYFAWEKNPSTILNPGHCGLSRSTG 154  
Qy 104 LREMFKYDCEQOHSFICKF 122  
Db 155 FLKMKDYNCDAKLPYICKF 173

Search completed: May 2, 2005, 16:02:54  
Job time : 26 secs